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OM nucleic - nucleic search, using sw model

Run on: December 13, 2003, 22:59:08; Search time 19949 Seconds  
(without alignments)  
11711.609 Million cell updates/sec

Title: US-09-923-327a-263  
Perfect score: 5711  
Sequence: 1 agctcgtgagacttctgg.....tccccacagccactactga 5711

Scoring table: IDENTITY NUC  
Gapop 10.0, Gapext 1.0

Searched: 2889711 seqs, 2045481386 residues

Total number of hits satisfying chosen parameters: 5777422

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : GenEmbl.\*

- 1: gb.ba.\*
- 2: gb.htg.\*
- 3: gb.in.\*
- 4: gb.om.\*
- 5: gb.ov.\*
- 6: gb.pat.\*
- 7: gb.ph.\*
- 8: gb.pl.\*
- 9: gb.pr.\*
- 10: gb.ro.\*
- 11: gb.sts.\*
- 12: gb.sy.\*
- 13: gb.un.\*
- 14: gb.vi.\*
- 15: em.ba.\*
- 16: em.fun.\*
- 17: em.hum.\*
- 18: em.in.\*
- 19: em.mu.\*
- 20: em.om.\*
- 21: em.or.\*
- 22: em.ov.\*
- 23: em.pat.\*
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- 33: em.htg.mus.\*
- 34: em.htg.pln.\*
- 35: em.htg.rod.\*
- 36: em.htg.mam.\*
- 37: em.htg.vrt.\*
- 38: em.sy.\*
- 39: em.htgo.hum.\*
- 40: em.htgo.mus.\*
- 41: em.htgo.other.\*

Pred. No. is the number of results predicted by chance to have a

score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	DB	ID	Description
1	5711	100.0	5711	6	AR007333	AR007333 Sequence
2	5711	100.0	5711	6	AR112808	AR112808 Sequence
3	5711	100.0	5711	6	I59546	I59546 Sequence 1
4	5709.4	100.0	5711	6	AR007335	AR007335 Sequence
5	5709.4	100.0	5711	6	AR112809	AR112809 Sequence
6	5701.4	99.8	5711	6	AR007334	AR007334 Sequence
7	5701.4	99.8	5711	6	AR112810	AR112810 Sequence
8	5699.8	99.8	5711	6	AR033056	AR033056 Sequence
9	5699.8	99.8	5711	6	AX659576	AX659576 Sequence
10	5699.8	99.8	5711	9	HSU14680	U14680 Homo sapien
11	5699.8	99.8	5712	6	AR070223	AR070223 Sequence
12	5699.8	99.8	5712	6	AR118507	AR118507 Sequence
13	5699.8	99.8	5712	6	AR125601	AR125601 Sequence
14	5699.8	99.8	5712	6	AR184044	AR184044 Sequence
15	5699.8	99.8	5914	6	AR004673	AR004673 Sequence
16	5699.8	99.8	5914	6	AR008159	AR008159 Sequence
17	5699.8	99.8	5914	6	AR136942	AR136942 Sequence
18	5699.8	99.8	5914	6	BD105583	BD105583 Genes sen
19	5699.8	99.8	5914	6	I76943	I76943 Sequence 1
20	5699.8	99.8	5914	6	I80938	I80938 Sequence 1
21	5699.8	99.8	5914	6	I81034	I81034 Sequence 1
22	5698.2	99.8	5711	6	AR048660	AR048660 Sequence
23	5698.2	99.8	5711	6	AR048666	AR048666 Sequence
24	5698.2	99.8	5711	6	AR278112	AR278112 Sequence
25	5698.2	99.8	5711	6	AR278118	AR278118 Sequence
26	5698.2	99.8	5711	6	I40795	I40795 Sequence 4
27	5698.2	99.8	5711	6	I40801	I40801 Sequence 10
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30	5688.8	99.6	5712	6	I40803	I40803 Sequence 12
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33	5687.8	99.6	5710	6	I40797	I40797 Sequence 6
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36	5685.8	99.6	5709	6	AR048664	AR048664 Sequence
37	5685.8	99.6	5709	6	AR048665	AR048665 Sequence
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39	5685.8	99.6	5709	6	AR278115	AR278115 Sequence
40	5685.8	99.6	5709	6	AR278116	AR278116 Sequence
41	5685.8	99.6	5709	6	AR278117	AR278117 Sequence
42	5685.8	99.6	5709	6	I40793	I40793 Sequence 2
43	5685.8	99.6	5709	6	I40798	I40798 Sequence 7
44	5685.8	99.6	5709	6	I40799	I40799 Sequence 8
45	5685.8	99.6	5709	6	I40800	I40800 Sequence 9

ALIGNMENTS

RESULT 1  
AR007333  
LOCUS  
DEFINITION Sequence 1 from patent US 5750400.  
ACCESSION AR007333  
VERSION AR007333.1 GI:3966817  
KEYWORDS  
SOURCE Unknown.  
ORGANISM Unclassified.  
REFERENCE 1 (bases 1 to 5711)  
AUTHORS Murphy,P.D., Allen,A.C., Alvares,C.P., Critz,B.S., Olson,S.J., Schelter,D.B. and Zeng,B.  
TITLE Coding sequences of the human BRCA1 gene  
JOURNAL Patent: US 5750400-A 1 12-MAY-1998;

5711 bp DNA linear PAT 04-DEC-1998

FEATURES		Location/Qualifiers	
source		1..5711	
BASE COUNT		1953 a 1099 c 1277 g 1382 t	
ORIGIN		/organism="unknown"	
Query Match		100.0%; Score 5711; DB 6; Length 5711;	
Best Local Similarity		100.0%; Pred. No. 0;	
Matches 5711; Conservative		0; Mismatches 0; Indels 0; Gaps 0;	
Qy	1	AGCTCGCTGAGACTTCCTGGACCCCGACACAGGCTGTGGGTTCTCAGATAACTGGGCC	60
Db	1	AGCTCGCTGAGACTTCCTGGACCCCGACACAGGCTGTGGGTTCTCAGATAACTGGGCC	60
Qy	61	CTGGGCTCAGGAGGCTTCACCTCTGCTCTGGGTAAAGTTCATTGGAACAGAAAGAA	120
Db	61	CTGGGCTCAGGAGGCTTCACCTCTGCTCTGGGTAAAGTTCATTGGAACAGAAAGAA	120
Qy	121	TGGATTTATGCTCTTCGCGTTGAAGAAAGTACAAATGTCAATTAATGCTATGCAGAAA	180
Db	121	TGGATTTATGCTCTTCGCGTTGAAGAAAGTACAAATGTCAATTAATGCTATGCAGAAA	180
Qy	181	TCCTAGAGTCCCATCTGCTCGAGTTGATCAAGGAACCTGTCTCCAAAGTGTGACC	240
Db	181	TCCTAGAGTCCCATCTGCTCGAGTTGATCAAGGAACCTGTCTCCAAAGTGTGACC	240
Qy	241	ACATATTTGCAAAATTTTGCACTGTGAACTTCTCAACCAGAAAGGGCTTCACAGT	300
Db	241	ACATATTTGCAAAATTTTGCACTGTGAACTTCTCAACCAGAAAGGGCTTCACAGT	300
Qy	301	GTCCTTTATGATGATATACCAAAAGGAGCTACAAAGAAAGTACGAGATTTAGTC	360
Db	301	GTCCTTTATGATGATATACCAAAAGGAGCTACAAAGAAAGTACGAGATTTAGTC	360
Qy	361	AACCTGTTGAGAGCTATTGAAATCAATTTGTGCTTTTCAGCTTGACAGAGTTGGAGT	420
Db	361	AACCTGTTGAGAGCTATTGAAATCAATTTGTGCTTTTCAGCTTGACAGAGTTGGAGT	420
Qy	421	ATGCAACAGCTATAATTTTCAAAAAGGAAATAACTCTCCCTGAACATCTAAAGATG	480
Db	421	ATGCAACAGCTATAATTTTCAAAAAGGAAATAACTCTCCCTGAACATCTAAAGATG	480
Qy	481	AAGTTTCTATCATCCAAAGTATGGCTACAGAAACCGTGCCAAAGACTTCTACAGAGTG	540
Db	481	AAGTTTCTATCATCCAAAGTATGGCTACAGAAACCGTGCCAAAGACTTCTACAGAGTG	540
Qy	541	AACCGAATTCCTTCCTGAGAAACCACTCTCAGTGTCCAACTCTCTAACCTTGAA	600
Db	541	AACCGAATTCCTTCCTGAGAAACCACTCTCAGTGTCCAACTCTCTAACCTTGAA	600
Qy	601	CTGTGAGAACTCTGAGGACAAAGCAGCGGATACAACTCTCAAAAGACGCTGTCTACATTG	660
Db	601	CTGTGAGAACTCTGAGGACAAAGCAGCGGATACAACTCTCAAAAGACGCTGTCTACATTG	660
Qy	661	AATTGGATCTGATTCCTTGAAGATACCGTTTAAAGGCAACTTATTGCAAGTGTGGAG	720
Db	661	AATTGGATCTGATTCCTTGAAGATACCGTTTAAAGGCAACTTATTGCAAGTGTGGAG	720
Qy	721	ATCAGAAATGTTTACAATCACCCCTCAGGAACCGGATGAAATCAGTTTGGATCTG	780
Db	721	ATCAGAAATGTTTACAATCACCCCTCAGGAACCGGATGAAATCAGTTTGGATCTG	780
Qy	781	CAAAAAGGCTGCTGTGAAATTTTCTGAGACGGATGTAACAAATPACTGAAATCATCAAC	840
Db	781	CAAAAAGGCTGCTGTGAAATTTTCTGAGACGGATGTAACAAATPACTGAAATCATCAAC	840
Qy	841	CCAGTAATATGATTTGAACACCACTGAGAGCGGTGAGGATCCAGAAAGT	900
Db	841	CCAGTAATATGATTTGAACACCACTGAGAGCGGTGAGGATCCAGAAAGT	900
Qy	901	ATCAGGCTGCTCTGTTTCAACTTGTGATGTGAGCCATGTGGCAAAATPACTCATGCCA	960
Db	901	ATCAGGCTGCTCTGTTTCAACTTGTGATGTGAGCCATGTGGCAAAATPACTCATGCCA	960

Qy	961	GCTCATTACAGCATGAGAACAGCAGTATTATTACTCTACTAAAGACAGAAATGAATGTAGAAA	1020
Db	961	GCTCATTACAGCATGAGAACAGCAGTATTATTACTCTACTAAAGACAGAAATGAATGTAGAAA	1020
Qy	1021	AGGCTGAATTCGTGTAATAAAGCAAAACAGCTGCTGTAGCAAGGAGCAACATACAGAT	1080
Db	1021	AGGCTGAATTCGTGTAATAAAGCAAAACAGCTGCTGTAGCAAGGAGCAACATACAGAT	1080
Qy	1081	GGGCTGGAAGTAAAGAAACATGTAAATGATAGGGGACTCCCGACACAGAAAAAGGTAG	1140
Db	1081	GGGCTGGAAGTAAAGAAACATGTAAATGATAGGGGACTCCCGACACAGAAAAAGGTAG	1140
Qy	1141	ATCTGAATGCTGATCCCTCTGTGTGAGAGAAAGATGGAATAGCAGAAAACTGCATGCT	1200
Db	1141	ATCTGAATGCTGATCCCTCTGTGTGAGAGAAAGATGGAATAGCAGAAAACTGCATGCT	1200
Qy	1201	CAGAGAAATCCTAGAGATATCTGAAGATGTTCTTGGATAACACTAAATAGCAGCAATTCAGA	1260
Db	1201	CAGAGAAATCCTAGAGATATCTGAAGATGTTCTTGGATAACACTAAATAGCAGCAATTCAGA	1260
Qy	1261	AAGTTAATGATGGTGTTCAGAAAGTGAATGAACCTGTTAGGTCTGTGATGACTCAGATG	1320
Db	1261	AAGTTAATGATGGTGTTCAGAAAGTGAATGAACCTGTTAGGTCTGTGATGACTCAGATG	1320
Qy	1321	GGGAGTCTGAATCAAAATGCCCAGAAAGTGAATGATGAGGCTTCTAAATGAGGTAGATG	1380
Db	1321	GGGAGTCTGAATCAAAATGCCCAGAAAGTGAATGATGAGGCTTCTAAATGAGGTAGATG	1380
Qy	1381	AAATATCTGCTGTTCTCAGAGAAATAGACTTACTTGGCCAGTGTCTCTCATGAGGCTTTAA	1440
Db	1381	AAATATCTGCTGTTCTCAGAGAAATAGACTTACTTGGCCAGTGTCTCTCATGAGGCTTTAA	1440
Qy	1441	TATGTAAAGTGAAGAGTTTCACTCCAAATCAGTGTAGAGATAATATTGAAGACAAAAATAT	1500
Db	1441	TATGTAAAGTGAAGAGTTTCACTCCAAATCAGTGTAGAGATAATATTGAAGACAAAAATAT	1500
Qy	1501	TTGGGAAACCTATCCGAGAGAGGAGCCCTCCCACTTAAAGCCATGTAACTGAAATATC	1560
Db	1501	TTGGGAAACCTATCCGAGAGAGGAGCCCTCCCACTTAAAGCCATGTAACTGAAATATC	1560
Qy	1561	TAATTTAGGAGCATTTGTTTACTGAGCCACAGATAATACAAAGAGCGTCCCTCACAATA	1620
Db	1561	TAATTTAGGAGCATTTGTTTACTGAGCCACAGATAATACAAAGAGCGTCCCTCACAATA	1620
Qy	1621	AATTAAGCGTAAAGAGACCTTACATCAGGCTTCTCATCTGAGGATTTTATCAAGAAAG	1680
Db	1621	AATTAAGCGTAAAGAGACCTTACATCAGGCTTCTCATCTGAGGATTTTATCAAGAAAG	1680
Qy	1681	CAGATTTGGCAGTTCAAAAGACTCCTGAAATGATAATCAGGAACTTAACCAACCGGAGC	1740
Db	1681	CAGATTTGGCAGTTCAAAAGACTCCTGAAATGATAATCAGGAACTTAACCAACCGGAGC	1740
Qy	1741	AGAATGGTCAAGTGAATGATTTTACTTAATAGTGTCTCATGAGATAAAACAAAAGGTGATT	1800
Db	1741	AGAATGGTCAAGTGAATGATTTTACTTAATAGTGTCTCATGAGATAAAACAAAAGGTGATT	1800
Qy	1801	CTATTGAGAAATGAGAAAAATCTTAAACCCCAATAGAACTACCTCGAAAAAGAAATCTGCTTCA	1860
Db	1801	CTATTGAGAAATGAGAAAAATCTTAAACCCCAATAGAACTACCTCGAAAAAGAAATCTGCTTCA	1860
Qy	1861	AAACGAAAGCTGAACCTTATAAGCAGCAGTATAGCAATATGGAACCTCGAATTAATATCC	1920
Db	1861	AAACGAAAGCTGAACCTTATAAGCAGCAGTATAGCAATATGGAACCTCGAATTAATATCC	1920
Qy	1921	ACAATTTCAAAAGCACCTTAAAAAGATAGGCTGAGGAGGAGTCTTCTACAGGCAATATTC	1980
Db	1921	ACAATTTCAAAAGCACCTTAAAAAGATAGGCTGAGGAGGAGTCTTCTACAGGCAATATTC	1980
Qy	1981	ATGCGCTTGAACCTAGTGTGAGTAAATCTTAAGCCCACTAATTTGTAATGAAATTCGAA	2040
Db	1981	ATGCGCTTGAACCTAGTGTGAGTAAATCTTAAGCCCACTAATTTGTAATGAAATTCGAA	2040

Qy	2041	TTGATAGTTGTTCTAGCAGTGAAGAGATAAAGAAAAAAGTACAAACAAATGCCAGTCA	2100
Db	2041	TTGATAGTTGTTCTAGCAGTGAAGAGATAAAGAAAAAAGTACAAACAAATGCCAGTCA	2100
Qy	2101	GGCAGCAGAGAAACCTACCACTCATGGAAGTAAAGAACCTGCAACTGGAGCCCAAGAGA	2160
Db	2101	GGCAGCAGAGAAACCTACCACTCATGGAAGTAAAGAACCTGCAACTGGAGCCCAAGAGA	2160
Qy	2161	GTAACAAGCCAAATGAAACAGACAAGTAAAGACATGACAGTGATCTTTCCAGAGCTGA	2220
Db	2161	GTAACAAGCCAAATGAAACAGACAAGTAAAGACATGACAGTGATCTTTCCAGAGCTGA	2220
Qy	2221	AGTTAAACAAATGCACCTGGTCTTTTACTAAGTGTCAAATACCAGTGAACCTTAAAGAT	2280
Db	2221	AGTTAAACAAATGCACCTGGTCTTTTACTAAGTGTCAAATACCAGTGAACCTTAAAGAT	2280
Qy	2281	TTGTCAATCTCTAGCCTTCCAGAGAGAGAAAGAGAGAACTAGAACAGTCTAAAGTGT	2340
Db	2281	TTGTCAATCTCTAGCCTTCCAGAGAGAGAAAGAGAGAACTAGAACAGTCTAAAGTGT	2340
Qy	2341	CTAATAATGCTGAAGACCCCAAGATCTCATGTTAAAGTGGAGAAAGGTTTTGCAAACTG	2400
Db	2341	CTAATAATGCTGAAGACCCCAAGATCTCATGTTAAAGTGGAGAAAGGTTTTGCAAACTG	2400
Qy	2401	AAAGATCTGTAGAGATGACGATATTTCACTGGTACCTGGTACTGATATATGGCACTCAGG	2460
Db	2401	AAAGATCTGTAGAGATGACGATATTTCACTGGTACCTGGTACTGATATATGGCACTCAGG	2460
Qy	2461	AAAGTATCTGTTACTGGAAGTTAGCACTCTAGGGAAGGCAAAACAGAACCAATAAAT	2520
Db	2461	AAAGTATCTGTTACTGGAAGTTAGCACTCTAGGGAAGGCAAAACAGAACCAATAAAT	2520
Qy	2521	GTGTGAGTCAGTGTGCAGCATTTGAAACCCCAAGGCACTAATTCATGGTTGTTCCAAAG	2580
Db	2521	GTGTGAGTCAGTGTGCAGCATTTGAAACCCCAAGGCACTAATTCATGGTTGTTCCAAAG	2580
Qy	2581	ATAATAGAAATGACACAGAAAGCTTTAAGTATCCATTGGGACATGAAGTTAACCAAGTC	2640
Db	2581	ATAATAGAAATGACACAGAAAGCTTTAAGTATCCATTGGGACATGAAGTTAACCAAGTC	2640
Qy	2641	GGGAAACAGCATAGAAATGGAAGAAAGTGAATTCATGCTGAGTATTCAGAAATACAT	2700
Db	2641	GGGAAACAGCATAGAAATGGAAGAAAGTGAATTCATGCTGAGTATTCAGAAATACAT	2700
Qy	2701	TCAAGGTTTCAAAGCGCCAGTCATTGCTCTGTTTTCAAATCCAGGAAATGCAGAGAGG	2760
Db	2701	TCAAGGTTTCAAAGCGCCAGTCATTGCTCTGTTTTCAAATCCAGGAAATGCAGAGAGG	2760
Qy	2761	AATGTGCAACATTTCTGCCCCACTCTGGTCTTTAAAGAAACAAAGTCCAAAAGTCACTT	2820
Db	2761	AATGTGCAACATTTCTGCCCCACTCTGGTCTTTAAAGAAACAAAGTCCAAAAGTCACTT	2820
Qy	2821	TTGAATGTGAACAAAGGAAGAAATCAAGAAAGATGAGTCTTAATATCAAGCTGTAC	2880
Db	2821	TTGAATGTGAACAAAGGAAGAAATCAAGAAAGATGAGTCTTAATATCAAGCTGTAC	2880
Qy	2881	AGACAGTTAATATCACTCAGGCTTTCTGTGTGTTGTCAGAAAGATGAAGCCAGTTGATA	2940
Db	2881	AGACAGTTAATATCACTCAGGCTTTCTGTGTGTTGTCAGAAAGATGAAGCCAGTTGATA	2940
Qy	2941	ATGCCAAATGTAGTATCAAAAGGAGCTCTAGGTTTTGTCTATCTCAGTTTCAGAGGCA	3000
Db	2941	ATGCCAAATGTAGTATCAAAAGGAGCTCTAGGTTTTGTCTATCTCAGTTTCAGAGGCA	3000
Qy	3001	ACGAAACTGGACTCATTTACTCCAAATAAATGAGACTTTTACAAAACCCATATCGTATAC	3060
Db	3001	ACGAAACTGGACTCATTTACTCCAAATAAATGAGACTTTTACAAAACCCATATCGTATAC	3060
Qy	3061	CACCACCTTTTCCCATCAAGTCATTGTTTAAACTTAAATGTAAGAAAAATCTGCTAGAGG	3120
Db	3061	CACCACCTTTTCCCATCAAGTCATTGTTTAAACTTAAATGTAAGAAAAATCTGCTAGAGG	3120
Qy	3121	AAAACTTTGAGGAACATTTCAATGTCACTGAAAGAGAAATGGGAAATGAGAACATTTCCAA	3180

Db	3121	AAAACTTTGAGGAACATTTCAATGTCACTGAAAGAGAAATGGGAAATGAGAACATTTCCAA	3180
Qy	3181	GTACAGTGTAGCACAATTTAGCGCTAATAACATTAGAGAAAAATGTTTTTAAAGGAGCCAGCT	3240
Db	3181	GTACAGTGTAGCACAATTTAGCGCTAATAACATTAGAGAAAAATGTTTTTAAAGGAGCCAGCT	3240
Qy	3241	CAAGCAATATAATTAAGATAGGTTCCAGTACTAATGAAGTGGGCTCCAGTATTAATGAAA	3300
Db	3241	CAAGCAATATAATTAAGATAGGTTCCAGTACTAATGAAGTGGGCTCCAGTATTAATGAAA	3300
Qy	3301	TAGTGTCCAGTGTAGAAAAATTTCAACAGCAGAACCTAGCTAGBAAACAGAGGGCCAAAATTGA	3360
Db	3301	TAGTGTCCAGTGTAGAAAAATTTCAACAGCAGAACCTAGCTAGBAAACAGAGGGCCAAAATTGA	3360
Qy	3361	ATGCTATGCTTAGATTAGGGGTTTTGCAACTGAGGCTCTATAAAACAAAGTCTTCTCTGAAA	3420
Db	3361	ATGCTATGCTTAGATTAGGGGTTTTGCAACTGAGGCTCTATAAAACAAAGTCTTCTCTGAAA	3420
Qy	3421	GTAATTTGAAAGCTCTGAAAATAAAGAACAGCAAGTATGAAGAAAGTGTTCAGACTGTGA	3480
Db	3421	GTAATTTGAAAGCTCTGAAAATAAAGAACAGCAAGTATGAAGAAAGTGTTCAGACTGTGA	3480
Qy	3481	ATACAGATTTCTCTCCATATCTGATTTTTCAGATACTTAGAACAGCTATGGAAGTGTCTC	3540
Db	3481	ATACAGATTTCTCTCCATATCTGATTTTTCAGATACTTAGAACAGCTATGGAAGTGTCTC	3540
Qy	3541	ATGCATCTCAGGTTGTTCTTGAGACACCTGATGACCTGTTAGATGATGGTCAAAATAAAGG	3600
Db	3541	ATGCATCTCAGGTTGTTCTTGAGACACCTGATGACCTGTTAGATGATGGTCAAAATAAAGG	3600
Qy	3601	AAGTACTAGTGTGCTGAAAATGACATTAAGGAAAGTTCGTCTGTTTTTAGCAAAAAGCG	3660
Db	3601	AAGTACTAGTGTGCTGAAAATGACATTAAGGAAAGTTCGTCTGTTTTTAGCAAAAAGCG	3660
Qy	3661	TCCAGAGAGGAGCTTAGCAGGAGTCTAGCCCTTTTCAACCATACACATTTGGCTCAGG	3720
Db	3661	TCCAGAGAGGAGCTTAGCAGGAGTCTAGCCCTTTTCAACCATACACATTTGGCTCAGG	3720
Qy	3721	GTTACCAAGAGGGGCCAAGAAATTTAGAGTCTCAGAGAGAACTTATCTAGTGAGGATG	3780
Db	3721	GTTACCAAGAGGGGCCAAGAAATTTAGAGTCTCAGAGAGAACTTATCTAGTGAGGATG	3780
Qy	3781	AAGAGCTTCCCTGCTTCCAAACATCTGTTATTTGGTAAAGTAAACAATACTCTCTCAGT	3840
Db	3781	AAGAGCTTCCCTGCTTCCAAACATCTGTTATTTGGTAAAGTAAACAATACTCTCTCAGT	3840
Qy	3841	CTACTAGGCATAGCACCGTTGCTACCGAGTGTCTGTCTAAGAAACACAGAGAGAAATTTAT	3900
Db	3841	CTACTAGGCATAGCACCGTTGCTACCGAGTGTCTGTCTAAGAAACACAGAGAGAAATTTAT	3900
Qy	3901	TATCATTTGAAGAAATAGCTTTAAATGCAGTGAACCAAGTAAATTTGSCAAAGGCATCTC	3960
Db	3901	TATCATTTGAAGAAATAGCTTTAAATGCAGTGAACCAAGTAAATTTGSCAAAGGCATCTC	3960
Qy	3961	AGGAACATCACTTTAGTGAGGAAACAAAATGTTCTGCTAGCTGTGTTTTCTTTCACAGTGA	4020
Db	3961	AGGAACATCACTTTAGTGAGGAAACAAAATGTTCTGCTAGCTGTGTTTTCTTTCACAGTGA	4020
Qy	4021	GTGAATTTGGAAGACTTGACTGCAAAATACAAACACCCAGGATCTTTCTTGTATTTGGTCTT	4080
Db	4021	GTGAATTTGGAAGACTTGACTGCAAAATACAAACACCCAGGATCTTTCTTGTATTTGGTCTT	4080
Qy	4081	CCAAACAAATGAGGCATCAGTCTGAAAGCCAGGAGTTGGTCTGAGTGACAGGAATTTGG	4140
Db	4081	CCAAACAAATGAGGCATCAGTCTGAAAGCCAGGAGTTGGTCTGAGTGACAGGAATTTGG	4140
Qy	4141	TTTCAGATGTATGAAGAAAGAGGAAACGGGCTTTGGAAGAAAAATAATCAAGAGAGCAAGCA	4200
Db	4141	TTTCAGATGTATGAAGAAAGAGGAAACGGGCTTTGGAAGAAAAATAATCAAGAGAGCAAGCA	4200
Qy	4201	TGGATTCAAACCTTAGGTGAAGCAGCATCTGGGTGTGAGAGTGAAACAAAGCGTCTCTGAAG	4260
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4261	Qy	ACTGCTCAGGGCTATCTCTCAGAGTGAACATTTTAAACCACTCAGCAGAGGATACCATGC	4320
4261	Db	ACTGCTCAGGGCTATCTCTCAGAGTGAACATTTTAAACCACTCAGCAGAGGATACCATGC	4320
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4321	Db	AACATAACTGATAAAGCTCCAGCAGGAATGGCTGAACCTAGAGCTGTGTAGAAACAGC	4380
4381	Qy	ATGGAGGCCAGCCTTCTAAAGCTTACCCCTCCATCATAACTGACTCCTCTGCCCTTGAGG	4440
4381	Db	ATGGAGGCCAGCCTTCTAAAGCTTACCCCTCCATCATAACTGACTCCTCTGCCCTTGAGG	4440
4441	Qy	ACCTGCCAATACTCAGAAACAAAGCACAACAGAAAAGCAGTATTAACTTCACAGAAAGTA	4500
4441	Db	ACCTGCCAATACTCAGAAACAAAGCACAACAGAAAAGCAGTATTAACTTCACAGAAAGTA	4500
4501	Qy	GTGAATACCTTATAAGCCAGAACTCCAGAGGCCCTTCTGCTGACAAGTTTGAGGCTGTCTG	4560
4501	Db	GTGAATACCTTATAAGCCAGAACTCCAGAGGCCCTTCTGCTGACAAGTTTGAGGCTGTCTG	4560
4561	Qy	CAGATAGTTCTACCGTAAATAAAGAACCCAGAGTGGAAAGGTCATCCCTTCTAAAT	4620
4561	Db	CAGATAGTTCTACCGTAAATAAAGAACCCAGAGTGGAAAGGTCATCCCTTCTAAAT	4620
4621	Qy	GCCCATCACTTAGATGATAGTGGTACATGACACAGTTGCTCTCGGAGTCTTTCAGAAATAGAA	4680
4621	Db	GCCCATCACTTAGATGATAGTGGTACATGACACAGTTGCTCTCGGAGTCTTTCAGAAATAGAA	4680
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4681	Db	ACTACCCATCTCAAGAGGAGCTCATTAAGGTTTGTGATGTGGAGGCAACAGCTGGAAG	4740
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4801	Db	CCCCCTACCTGGAACTCGGAATCAGGCTCTTCTGTATGACCCCTGAACTCTGATCCTTCG	4860
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5041	Db	CTTCAACAGAAAGGGTCAAACAAAGAAATGTCCATGTGTGTCTGGCTGACCCAGAG	5100
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5161	Db	CTGAAGAGACTACTCATGTTGTTATGAAACAGATGCTGAGTTTGTGTGTAACGACAC	5220
5221	Qy	TGAAATATTTTCTAGGAATTCGGGAGGAAATGGGTAGTTAGCTATTTTCTGGGTGACCC	5280
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Db	5701	GCACACTACTGA 5711	

RESULT 2  
ARL12808

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LOCUS           ARL12808                               5711 bp      DNA          linear   PAR 16-MAY-2001
DEFINITION     Sequence 1 from patent US 6130322.
ACCESSION     AR112808
VERSION       AR112808.1 GI:114092708
KEYWORDS
SOURCE        unknown.
ORGANISM      Unclassified.
REFERENCE     1 (bases 1 to 5711)
AUTHORS      Murphy,P.D., Allen,A.C.P., Alvares,C.P., Critz,B.S., Olson,S.J.,
              Thurber,D. and Zeng,B.
TITLE        Coding sequences of the human BRCA1 gene
JOURNAL      Patent: US 6130322-A 1 10-OCT-2000;
FEATURES             Location/Qualifiers
source         1..5711
               /organism="unknown"

BASE COUNT    1953 a 1099 c 1277 g 1382 t
ORIGIN
Query Match    100.0%; Score 5711; DB 6; Length 5711;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 5711; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy 241 ACATATTTTGCAAATTTTGCATGCTGAAACTTCTCAACACAGAAAGAAAGGCCCTTCACAGT 300

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Qy 5701 GCCACTACTGA 5711  
Db 5701 GCCACTACTGA 5711

RESULT 3  
159546  
LOCUS  
DEFINITION Sequence 1 from patent US 5654155.  
ACCESSION 159546  
VERSION 159546.1 GI:2478178  
KEYWORDS  
SOURCE Unknown.  
ORGANISM Unknown.  
REFERENCE 1 (bases 1 to 5711)  
AUTHORS Murphy, P.D., Allen, A.C., Alvares, C.P., Critz, B.S., Olson, S.J.,  
Schelker, D.B. and Zeng, B.  
TITLE Consensus sequence of the human BRCA1 gene  
JOURNAL Patent: US 5654155-A 1 05-AUG-1997;  
FEATURES Location/Qualifiers  
source 1..5711  
BASE COUNT 1953 a 1099 c 1277 g 1382 t  
ORIGIN

Query Match 100.0%; Score 5711; DB 6; Length 5711;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 5711; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
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Ds	2881	AGACAGTTAATATCACTGCAGGCTTTCTGTGGTGGTTCAGAAAGATAAGCCAGTTGATA	2940
Qy	2941	ATGCAAAATGATGATCAAAAGAGGCTCTAGTGTGTTGTTCTATCATCTCAGTTTCAGAGGCA	3000
Ds	2941	ATGCAAAATGATGATCAAAAGAGGCTCTAGTGTGTTGTTCTATCATCTCAGTTTCAGAGGCA	3000
Qy	3001	ACGAAATCGGACTCAITTAATCAAAATAAACAATGGAATTTTACAAAACCCATATCGTATAC	3060
Ds	3001	ACGAAATCGGACTCAITTAATCAAAATAAACAATGGAATTTTACAAAACCCATATCGTATAC	3060
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Ds	3061	CACACATTTTCCCATCAAGTCATTTGTTAAATCTAAATGTAAGAAAATCTGCTAGAGG	3120
Qy	3121	AAAACTTTGAGGAACATTTCAATGTCACCTGAAGAGAAATGGGAAATGGAACAAATTC	3180
Ds	3121	AAAACTTTGAGGAACATTTCAATGTCACCTGAAGAGAAATGGGAAATGGAACAAATTC	3180
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Ds	3181	GACAGTGAGCACAAATAGCCGTAATAACATTTAGAGAAAATGTTTTAAAGAGGCCAGCT	3240
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Ds	3241	CAAGCAATTAATGAAGTAGGTTCCAGTACTAATGAAGTGGGCTCCAGTATTAATGA	3300
Qy	3301	TAGGTTCCAGTGATGAACAAATCAAGCAGAACTAGGTAGAAACAGAGGCGCAAAATGA	3360
Ds	3301	TAGGTTCCAGTGATGAACAAATCAAGCAGAACTAGGTAGAAACAGAGGCGCAAAATGA	3360
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Ds	3361	ATGCTATGCTTAGATTAGGGGTTTTGCAACCTGAGGCTATAAAACAAAGTCTTCTCTGGAA	3420
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Ds	3421	GTAATGTAAGCATCTCGAAATAAAAGCAAGAAATATGAAGAGTAGTTCAGACTGTTA	3480
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Ds	3481	ATACAGATTTCTCCATATCTGATTTTCAGATTAATAGACAGCCTATGGGAGTAGTC	3540
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Ds	3541	ATGCATCTCAGGTTGTTCTGAGACACCTGATGACCTGTTAGATGATGGTCAAAATAAAGG	3600
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Ds	3601	AAGATACATGTTTCTGAAATAAGCAATTAAGGAAAGTTCTGCTGTTTTTACGAAAAGCG	3660
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Ds	3661	TCCAGAGGAGAGCTTAGCAGGAGTCTAGCCCTTTACCCATACACATTTGGCTCAGG	3720
Qy	3721	GTTACCGAAGAGGGGCCAAGAAATAGAGTCTCTCAGAGAGAACTTATCTAGTCAGGATG	3780
Ds	3721	GTTACCGAAGAGGGGCCAAGAAATAGAGTCTCTCAGAGAGAACTTATCTAGTCAGGATG	3780
Qy	3781	AAGAGCTTCCCTGCTTCCAACTGTTTATTTGGTAAAGTAAACAAATATACCTTCTCAGT	3840
Ds	3781	AAGAGCTTCCCTGCTTCCAACTGTTTATTTGGTAAAGTAAACAAATATACCTTCTCAGT	3840
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Ds	3841	CTACTAGGATAGCACCGTTGCTACCGAGTGTCTGTCTTAAGAAACACAGAGGAGATTTAT	3900
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Ds	3901	TATCAATCAAGAAATAGCTTAAATGACTGCTAGTAAACAGGTAATTTGGCAAGGATCTC	3960
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Ds	4081	CCAAACAAATGAGGCATCAGTCTGAAAGCCAGGAGTTGGTCTGAGTCACAAGAAATGG	4140
Qy	4141	TTTCAGATGATGAAGAAAGGAGCGGCTTGGAGAAATAATCAAGAGAGCAAGCA	4200
Ds	4141	TTTCAGATGATGAAGAAAGGAGCGGCTTGGAGAAATAATCAAGAGAGCAAGCA	4200
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Ds	4261	ACTGCTCAGGCTATCTCTCAGAGTGCATTTTAAACCACTCAGCAGAGGATACCATGC	4320
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Ds	4381	ATGGAGCCAGGCTTTCTAAACAGCTACCTTCCATCATAAGTGACTCTCTGCCCTTGAGG	4440
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Ds	4501	GTGAATACCTTATTAAGCCAGAAATCCAGAAAGGCTTTCTGCTGACAAAGTCTGAGTGTCTG	4560
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Ds	4561	CAGATAGTTCTTACCAAGTAAATAAAGAACACAGAGTGGAAGGTCTATCCCTTCTTAAT	4620
Qy	4621	GCCCATCATTAGATGATGTTGATGCAAGTCTCTGGAGTCTTTCAGAAATAGAA	4680
Ds	4621	GCCCATCATTAGATGATGTTGATGCAAGTCTCTGGAGTCTTTCAGAAATAGAA	4680
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Ds	4681	ACTACCATCTCAAGAGGAGCTCAATTAAGTGTGTTGATGCGAGGAGCAACAGCTGGAG	4740
Qy	4741	AGTCTGGGCCACAGATTTGACGGAACATCTTACTTGCAGAGCAAGATCTAGAGGAA	4800
Ds	4741	AGTCTGGGCCACAGATTTGACGGAACATCTTACTTGCAGAGCAAGATCTAGAGGAA	4800
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Ds	4801	CCCCCTTACCTGGAATCTGGAATCAGCCTTCTCTGATGACCCCTGATCTGATCTCTG	4860
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Qy	5041	CTTCAACAGAAAGGCTCAACAAAGAAATGTCATGGTGGTCTGCTGGCTGACCCCAAG	5100
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RESULT 4	AR007335	AR007335	Sequence 5	7511 bp	DNA	linear	PAT 04-DEC-1998
LOCUS	AR007335	Sequence 5	from patent US 5750400.				
DEFINITION	AR007335	Sequence 5	from patent US 5750400.				
ACCESSION	AR007335	Sequence 5	from patent US 5750400.				
VERSION	AR007335.1	GI:3966819					
KEYWORDS							
SOURCE		Unknown.					
ORGANISM		Unknown.					
REFERENCE		Unclassified.					
AUTHORS		1 (bases 1 to 5711)					
		Murphy, P.D., Allen, A.C., Alvares, C.P., Critz, B.S., Olson, S.J.,					
		Schelter, D.B. and Zeng, B.					
TITLE		Coding sequences of the human BECAL gene					
JOURNAL		Patent: US 5750400-A 5 12-MAY-1998;					
FEATURES		Location/Qualifiers					
source		1..5711					
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BASE COUNT		1953 a 1098 c 1277 g 1383 t					
ORIGIN							
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ACCESSION AR112809  
VERSION AR112809.1 GI:14092709  
KEYWORDS  
SOURCE Unknown.  
ORGANISM Unknown.  
REFERENCE 1 (bases 1 to 5711)  
AUTHORS Murphy, P.D., Allen, A.C.P., Alvares, C.P., Critz, B.S., Olson, S.J.,  
Thurber, D. and Zeng, B.  
TITLE Coding sequences of the human BRCA1 gene  
JOURNAL Patent: US 6130322-A 3 10-OCT-2000;  
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BASE COUNT 1953 a 1098 c 1277 g 1383 t  
ORIGIN

Query Match 100.0%; Score 5709.4; DB 6; Length 5711;  
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Db	4441	ACCTGCGAAATCCAGAACAAAGCACATCAGAAAAAGCAGTATTAACTTCACAGAAAAAGTA	4500
Qy	4501	GTGAATACCTTATAAGCCAGNAATCCAGAGGCCCTTTCTGCTGACAAAGTTTGAGGTGTCTG	4560
Db	4501	GTGAATACCTTATAAGCCAGNAATCCAGAGGCCCTTTCTGCTGACAAAGTTTGAGGTGTCTG	4560
Qy	4561	CAGATAGTCTTACCAGTAAAAATAAGAAACAGAGGTGGAAAGGTCAATCCCTTCTTAAT	4620
Db	4561	CAGATAGTCTTACCAGTAAAAATAAGAAACAGAGGTGGAAAGGTCAATCCCTTCTTAAT	4620
Qy	4621	GCCCATCATTAGATGATAGGTGGTACATGCAAGTTGCTCTGCGAGTCTTTCAGAATAGAA	4680
Db	4621	GCCCATCATTAGATGATAGGTGGTACATGCAAGTTGCTCTGCGAGTCTTTCAGAATAGAA	4680
Qy	4681	ACTACCCATCTCAAGAGAGCTCATTAAGGTTGTTGATGTGGAGGACCAACAGCTGGAAG	4740
Db	4681	ACTACCCATCTCAAGAGAGCTCATTAAGGTTGTTGATGTGGAGGACCAACAGCTGGAAG	4740
Qy	4741	AGTCTGGGCCACAGATTTGACGAAACATCTTACTTTCCCAAGCAAGATCTAGAGGAA	4800
Db	4741	AGTCTGGGCCACAGATTTGACGAAACATCTTACTTTCCCAAGCAAGATCTAGAGGAA	4800
Qy	4801	CCCCCTTACCTGGAATCTGGAATCAGCCTCTTCTCTGATGACCCCTGGAATCTGATCTCTG	4860

[illegible]

RESULT 6

AR007334

## LOCUS

### DEFINITION

**ACCESSION**

VERSION

**KEYWORDS**  
**COLLAGE**

SOURCE  
ORGANIZATION

ORGANIZATION

AR007334 5711 bp DNA linear PAT 04-DEC-1998  
Sequence 3 from patent US 5750400.

AR007334  
AR007334.1 GI:3966818

Unknown.

**\*\*\*\*\***

AR007334	5711 bp	DNA	linear	PAT 04-DEC-1998
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Unclassified.									
1 (bases 1 to 5711)									
REFERENCE	Murphy, P.D., Allen, A.C., Alvares, C.P., Critz, B.S., Olson, S.J.,								
AUTHORS	Schelter, D.B. and Zeng, B.								
TITLE	Coding sequences of the human BRCA1 gene								
JOURNAL	Patent: US 5750400-A 3 12-MAY-1998;								
FEATURES	Location/Qualifiers								
source	1..5711								
BASE COUNT	1956 a 1098 c 1274 g 1383 t								
ORIGIN	/organism="unknown"								
Query Match	99.8%; Score 5701.4; DB 6; Length 5711;								
Best Local Similarity	99.9%; Pred. No. 0;								
Matches 5705; Conservative	0; Mismatches 5; Indels 0; Gaps 0;								
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QY	61	CCTCGCTCAGAGGSCCTTCAACCTCTGCTCTGGGTAAAGTTCAATGGAA	CAGAA	120					
Db	61	CCTCGCTCAGAGGSCCTTCAACCTCTGCTCTGGGTAAAGTTCAATGGAA	CAGAA	120					
QY	121	TGGATTATCTGCTCTTCGCGTTGAAGAAAGTACAAAATGTCAATTAATCT	TATGCA	180					
Db	121	TGGATTATCTGCTCTTCGCGTTGAAGAAAGTACAAAATGTCAATTAATCT	TATGCA	180					
QY	181	TCTTAGAGTCCCATCTGCTGAGTTGATCAAGAACCTGTCTCCAAAGTGT	GAAC	240					
Db	181	TCTTAGAGTCCCATCTGCTGAGTTGATCAAGAACCTGTCTCCAAAGTGT	GAAC	240					
QY	241	ACATATTTGCAAAATTTTGCAATGCTGAACTTCTCAACAGAAAGGCGCTT	CAAGT	300					
Db	241	ACATATTTGCAAAATTTTGCAATGCTGAACTTCTCAACAGAAAGGCGCTT	CAAGT	300					
QY	301	GTCTTTATGTAAGATGATATAACCAAAAGGAGCCTACAAAGAAAGTAC	GAGATTAGT	360					
Db	301	GTCTTTATGTAAGATGATATAACCAAAAGGAGCCTACAAAGAAAGTAC	GAGATTAGT	360					
QY	361	AACCTTTGAAAGCTATTTGAAATCATTTGTGCTTTTACGCTTGACAG	AGTTGGAGT	420					
Db	361	AACCTTTGAAAGCTATTTGAAATCATTTGTGCTTTTACGCTTGACAG	AGTTGGAGT	420					
QY	421	ATGCAAAACAGCTATAATTTTCCAAAAGGAAATAACTCTCCTGAA	CATCTAAAGNTG	480					
Db	421	ATGCAAAACAGCTATAATTTTCCAAAAGGAAATAACTCTCCTGAA	CATCTAAAGNTG	480					
QY	481	AAAGTTTCTATCATCCAAAGTATGGCTACAGAAACCGTGCCAAAGAC	CTTCTACAGAGTG	540					
Db	481	AAAGTTTCTATCATCCAAAGTATGGCTACAGAAACCGTGCCAAAGAC	CTTCTACAGAGTG	540					
QY	541	AACCCGAAATCCTTCTTGAGGAAACAGCTCTCAGTGTCCAACTCT	CTAAACCTTGAA	600					
Db	541	AACCCGAAATCCTTCTTGAGGAAACAGCTCTCAGTGTCCAACTCT	CTAAACCTTGAA	600					
QY	601	CTGTGAGAACTCTCAGGACAAAGCAGCGGTACAACTCTCAAAAG	ACCTCTGTACATTG	660					
Db	601	CTGTGAGAACTCTCAGGACAAAGCAGCGGTACAACTCTCAAAAG	ACCTCTGTACATTG	660					
QY	661	AATTGGGATCTGATTTCTTGAAGATACCGTTAATAAGGCAACTT	ATTGCAAGTGTGGAG	720					
Db	661	AATTGGGATCTGATTTCTTGAAGATACCGTTAATAAGGCAACTT	ATTGCAAGTGTGGAG	720					
QY	721	ATCAAGAAATTTGTAACAAATCAACCTCAAGGAAACAGGATGAA	ATCAGTTTGTCTG	780					
Db	721	ATCAAGAAATTTGTAACAAATCAACCTCAAGGAAACAGGATGAA	ATCAGTTTGTCTG	780					
QY	781	CAAAAAGGCTGCTTGTGAATTTTCTGAGCGGATGTAACAAAT	PACCTCAATCAAC	840					
Db	781	CAAAAAGGCTGCTTGTGAATTTTCTGAGCGGATGTAACAAAT	PACCTCAATCAAC	840					
QY	841	CCAGTAATATGATTTGAACCACTGAGAGCGGTGACGCTGAGAGG	CATCCGAAAGT	900					

Db	841	CCAGTAATATGATTTGAACCACTGAGAGCGGTGAGCTGAGGGCATCCGAA	AGT	900					
QY	901	ATCAGGGTAGTTCTGTTTCAAACTTGGATGTGGAGCCATGTGGCACA	AAATACTCATGCCA	960					
Db	901	ATCAGGGTAGTTCTGTTTCAAACTTGGATGTGGAGCCATGTGGCACA	AAATACTCATGCCA	960					
QY	961	GCTCATTACAGCATGAGACAGCAGTTTATTACTCATTAAAGACAG	AATGATGTAGAAA	1020					
Db	961	GCTCATTACAGCATGAGACAGCAGTTTATTACTCATTAAAGACAG	AATGATGTAGAAA	1020					
QY	1021	AGGCTGAATTTCTGTAATAAAAGCAACAGCTGCTTAGCAAGGAG	CAACATACAGAT	1080					
Db	1021	AGGCTGAATTTCTGTAATAAAAGCAACAGCTGCTTAGCAAGGAG	CAACATACAGAT	1080					
QY	1081	GGGCTGGAAGTAAGCAACATGTAATGATAGGCGGACTCCAGCA	CAAGAAAAGGTAG	1140					
Db	1081	GGGCTGGAAGTAAGCAACATGTAATGATAGGCGGACTCCAGCA	CAAGAAAAGGTAG	1140					
QY	1141	ATCTGAATGCTGATCCCTGTGTGAGAGAAAGAAATGGAATAG	CAGAAAATGCTGCT	1200					
Db	1141	ATCTGAATGCTGATCCCTGTGTGAGAGAAAGAAATGGAATAG	CAGAAAATGCTGCT	1200					
QY	1201	CAGAGAAATCCTAGAGATACCTGAAGATGTTCTTGGATAACACT	AAATAGCAGCATTCAGA	1260					
Db	1201	CAGAGAAATCCTAGAGATACCTGAAGATGTTCTTGGATAACACT	AAATAGCAGCATTCAGA	1260					
QY	1261	AAAGTTAATGATGTTTCCAGAAAGTGAATGATGATGATGATG	ATGATGATGATGATG	1320					
Db	1261	AAAGTTAATGATGTTTCCAGAAAGTGAATGATGATGATGATG	ATGATGATGATGATG	1320					
QY	1321	GGGAGTCTGAATCAAAATGCGCAAGTACGATGATGATGATG	ATGATGATGATGATG	1380					
Db	1321	GGGAGTCTGAATCAAAATGCGCAAGTACGATGATGATGATG	ATGATGATGATGATG	1380					
QY	1381	AAATATCTGCTTCTCAGAGAAATAGACTTACTGGCCAGTGC	CTCATGAGGCTTTAA	1440					
Db	1381	AAATATCTGCTTCTCAGAGAAATAGACTTACTGGCCAGTGC	CTCATGAGGCTTTAA	1440					
QY	1441	TATGTAAAGTGAAGAGTTCACTCCAAATCAGTAGAGATTAAT	TATTTGAAGACAAAATAT	1500					
Db	1441	TATGTAAAGTGAAGAGTTCACTCCAAATCAGTAGAGATTAAT	TATTTGAAGACAAAATAT	1500					
QY	1501	TTGGGAAACCTATCGGAAGAGCGAGCTCCCACTTAAGCCAT	GTAACTGAAAATC	1560					
Db	1501	TTGGGAAACCTATCGGAAGAGCGAGCTCCCACTTAAGCCAT	GTAACTGAAAATC	1560					
QY	1561	TAATATAGGAGCATTTGTTACTGAGCCACAGATAATACAAG	AGCGTCCCTCACAATA	1620					
Db	1561	TAATATAGGAGCATTTGTTACTGAGCCACAGATAATACAAG	AGCGTCCCTCACAATA	1620					
QY	1621	AATTAAGCGTAAAGAGACCTACATCAGGCTTCACTCTGAG	AGTATTTATCAAGAAAG	1680					
Db	1621	AATTAAGCGTAAAGAGAGACCTACATCAGGCTTCACTCTGAG	AGTATTTATCAAGAAAG	1680					
QY	1681	CAGATTGGCAGTTCAAAAGACTCCCTGAATGATTAATCAG	GAACCTAAACCAACGAGC	1740					
Db	1681	CAGATTGGCAGTTCAAAAGACTCCCTGAATGATTAATCAG	GAACCTAAACCAACGAGC	1740					
QY	1741	AGAATGGTCAAGTGAATATTTACTAATAGTGGTCAATGAG	AAATAAACAAGAGTCAAT	1800					
Db	1741	AGAATGGTCAAGTGAATATTTACTAATAGTGGTCAATGAG	AAATAAACAAGAGTCAAT	1800					
QY	1801	CTATTGAGATGAGAAAATCTTAACCCAAATAGAACTAC	CTCGAAAAGAAATCTGCTTCA	1860					
Db	1801	CTATTGAGATGAGAAAATCTTAACCCAAATAGAACTAC	CTCGAAAAGAAATCTGCTTCA	1860					
QY	1861	AAAGGAAAGCTGACCTTATAAGCAGCAGATTAAGCAAT	ATAGGAATCGAATTAATATCC	1920					
Db	1861	AAAGGAAAGCTGACCTTATAAGCAGCAGATTAAGCAAT	ATAGGAATCGAATTAATATCC	1920					
QY	1921	ACAATTCAAAAGCACTTAAAGAAATAGGCTGAGGAGGAG	AGTCTTCTTACCGGCAATTC	1980					
Db	1921	ACAATTCAAAAGCACTTAAAGAAATAGGCTGAGGAGGAG	AGTCTTCTTACCGGCAATTC	1980					



Db 1921 ACAATTTCAAAGCACCTAAAGAAGATAGGCTGAGGAGGAAGTCTTCTACAGGCATATTC 1980  
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Db 1981 ATGCGCTGGAATAGTAGTCAAGTGAAGAACTAAAGCCCACTAAATGTGTAAGTTCGAA 2040  
Qy 2041 TTGATAGTTGTTCTAGCAGTGAAGAGATAGAGAAAGAAAGTACAAACCAATGCCAGTCA 2100  
Db 2041 TTGATAGTTGTTCTAGCAGTGAAGAGATAGAGAAAGAAAGTACAAACCAATGCCAGTCA 2100  
Qy 2101 GGCAAGAGAGAAACCTACAACTCATGGAAGGTAAAGAACCTGCAACTGGAGCCCAAGAGA 2160  
Db 2101 GGCAAGAGAGAAACCTACAACTCATGGAAGGTAAAGAACCTGCAACTGGAGCCCAAGAGA 2160  
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Db 5701 GCCACTACTGA 5711

RESULT 7  
AR112810  
LOCUS AR112810 5711 bp DNA linear PAT 16-MAY-2001  
DEFINITION Sequence 5 from patent US 6130322.  
ACCESSION AR112810  
VERSION AR112810.1 GI:14092710  
KEYWORDS  
SOURCE Unknown.  
ORGANISM Unknown.  
REFERENCE 1 (bases 1 to 5711)  
AUTHORS Murphy, P.D., Allen, A.C.P., Alvares, C.P., Critz, B.S., Olson, S.J.,  
Thurber, D. and Zeng, B.  
TITLE Coding sequences of the human BRCA1 gene  
JOURNAL Patent: US 6130322-A 5 10-OCT-2000;  
FEATURES Location/Qualifiers  
source 1. 5711  
BASE COUNT 1956 a 1098 c 1274 g 1383 t  
ORIGIN

Query Match 99.8%; Score 5701.4; DB 6; Length 5711;  
Best Local Similarity 99.9%; Pred. No. 0;  
Matches 5705; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

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Db 61 CTTGCGCTCAGGAGGCTTCAACCTCTGCTGTGGTAAAGTTCATTGGAACAGAGAA 120  
Qy 121 TGAATTTATCTGCTTCTCGGCTTGAAGAGTACAAAATGTCAATTAATGCTATGCAGAAA 180  
Db 121 TGAATTTATCTGCTTCTCGGCTTGAAGAGTACAAAATGTCAATTAATGCTATGCAGAAA 180

181 TCCTAGAGTGCCCATCTGTCTGGAGTTGATCAAGGAACCTGTCTCCACAAGTGTGACC 240 Qy  
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ACCESSION AR033056  
VERSION AR033056.1 GI:5948661  
KEYWORDS  
SOURCE Unknown.  
ORGANISM Unknown.  
REFERENCE 1 (bases 1 to 5711)  
AUTHORS Yeung,A.T.  
TITLE Mismatch endonuclease and its use in identifying mutations in targeted polynucleotide strands  
JOURNAL Patent: US 5869245-A 1 09-FEB-1999;  
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VERSION AX659576.1 GI:29161780
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
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REFERENCE 1
AUTHORS dalla Venezia,N., Magnard,C., Lenoir,G. and Sinilnikova-Erard,O.
TITLE Brcal/acc alpha molecular complexes, diagnostic and therapeutic
applications
JOURNAL Patent: WO 02100897-A 15 19-DEC-2002;
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TITLE A strong candidate for the breast and ovarian cancer susceptibility gene BRCA1				
JOURNAL Science 266 (5182), 66-71 (1994)				
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PUBMED 7545954				
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AUTHORS Skolnick, M.H.				
TITLE Direct Submission				
JOURNAL Submitted (14-SEP-1994) Mark H. Skolnick, Myriad Genetics Inc. and the University of Utah, 421 Wakara Way, Suite 201, Salt Lake City, UT 84108, USA				
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RESULT 11  
AR070223  
LOCUS  
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ACCESSION  
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AR070223 5712 bp DNA linear PAT 18-FEB-2000  
Sequence 1 from patent US 5891857.  
AR070223  
AR070223.1 GI:7221111

KEYWORDS Unknown.  
SOURCE Unknown.  
ORGANISM Unclassified.  
REFERENCE 1 (bases 1 to 5712)  
AUTHORS Holt, J.T., Jensen, R.A., King, M.-C., Page, D.L., Szabo, C.I.,  
Jeton, I.D., Robinson-Benton, C.L. and Thompson, M.E.  
TITLE Characterized BRCA1 and BRCA2 proteins and screening and  
therapeutic methods based on characterized BRCA1 and BRCA2 proteins  
JOURNAL Patent: US 5891857-A 1 06-APR-1999;  
FEATURES Location/Qualifiers  
source 1..5712  
BASE COUNT 1956 a 1099 c 1274 g 1383 t  
ORIGIN  
Query Match 99.8%; Score 5699.8; DB 6; Length 5712;  
Best Local Similarity 99.9%; Pred. No. 0;  
Matches 5704; Conservative 0; Mismatches 7; Indels 0; Gaps 0;  
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Qy	1921	ACAAATCAAAAGCACCTAAAAAAGATAGGCTGAGGAGAAAGTCTTTACACAGGCATATTC	1980
Db	1921	ACAATTCAAAAGCACCTAAAAAAGATAGGCTGAGGAGAAAGTCTTTACACAGGCATATTC	1980
Qy	1981	ATGGGCTTGAACCTAGTAGTCAGTAGAATCTTAAGCCCAACCTAATTGTGTACTGAATTGCAAA	2040
Db	1981	ATGGGCTTGAACCTAGTAGTCAGTAGAATCTTAAGCCCAACCTAATTGTGTACTGAATTGCAAA	2040
Qy	2041	TTGATAGTTGTTCTTAGCAGTGAACAGAGATAAGAGAAAAGAAAGTCAACAACCAANTGCCAGTCA	2100
Db	2041	TTGATAGTTGTTCTTAGCAGTGAACAGAGATAAGAGAAAAGAAAGTCAACAACCAANTGCCAGTCA	2100
Qy	2101	GGCACAGCAGAAACCTCAACTCATGGAAGGTAAAGAAACCTGCAACTGGAGCCAAAGAAGA	2160
Db	2101	GGCACAGCAGAAACCTCAACTCATGGAAGGTAAAGAAACCTGCAACTGGAGCCAAAGAAGA	2160
Qy	2161	GTAAACAAGCCAAATGAAACAGACAAGTAAAGACAATGACATGATCTTTCCAGAGAGCTGA	2220
Db	2161	GTAAACAAGCCAAATGAAACAGACAAGTAAAGACAATGACATGATCTTTCCAGAGAGCTGA	2220
Qy	2221	AGTTAAACAAATGCACCTGGTCTTTTACTAAGTGTTCAAATACACAGTGAACCTTAAAGAAT	2280
Db	2221	AGTTAAACAAATGCACCTGGTCTTTTACTAAGTGTTCAAATACACAGTGAACCTTAAAGAAT	2280
Qy	2281	TTGTCAATCTTAGCTTCCAAAGAGAGAAAGAAAGAAAGTAAAGTAAAGTAAAGTGT	2340
Db	2281	TTGTCAATCTTAGCTTCCAAAGAGAGAAAGAAAGAAAGTAAAGTAAAGTAAAGTGT	2340
Qy	2341	CTAATAATGTCTGAAGACCCCAAGATCTCATGTTAAGTGGAGAAAGGGTTTTGCCAAACTG	2400
Db	2341	CTAATAATGTCTGAAGACCCCAAGATCTCATGTTAAGTGGAGAAAGGGTTTTGCCAAACTG	2400
Qy	2401	AAAGATCTGTAGAGAGTAGCAGTATTTCTAGTGTACCTGGTACTGTATATGGCACTCAGG	2460
Db	2401	AAAGATCTGTAGAGAGTAGCAGTATTTCTAGTGTACCTGGTACTGTATATGGCACTCAGG	2460
Qy	2461	AAAGTATCTCGTTACTGGAGTTAGCACTCTAGGGAAGGCAAAACAGAACCAAAATAAAT	2520
Db	2461	AAAGTATCTCGTTACTGGAGTTAGCACTCTAGGGAAGGCAAAACAGAACCAAAATAAAT	2520
Qy	2521	GTGTGAGTCAAGTGTGCAGCACTTTGAAAACCCCAAGGGAATAATCATGGTGTGTTCCAAAG	2580
Db	2521	GTGTGAGTCAAGTGTGCAGCACTTTGAAAACCCCAAGGGAATAATCATGGTGTGTTCCAAAG	2580
Qy	2581	ATAATAGAAATGACACAGAGGCTTTAAGTATCCATTTGGGACATGAAGTTAACCAAGT	2640
Db	2581	ATAATAGAAATGACACAGAGGCTTTAAGTATCCATTTGGGACATGAAGTTAACCAAGT	2640
Qy	2641	GGGAAAACAGCATAGAATGGAAGAAAGTGAACCTTGATGTCTCAGTATTTCCAGAAATACAT	2700
Db	2641	GGGAAAACAGCATAGAATGGAAGAAAGTGAACCTTGATGTCTCAGTATTTCCAGAAATACAT	2700
Qy	2701	TCAGGTTTCAAAGCGCCAGTCAATTTGCTCTGTGTTTTCAAATCCAGGAAAATGCGAGAGAGG	2760
Db	2701	TCAGGTTTCAAAGCGCCAGTCAATTTGCTCCGTGTTTTCAAATCCAGGAAAATGCGAGAGAGG	2760
Qy	2761	AATGTGACAAATCTCTGCCCACTCTCGGGTCTTTAAAGAAACAAAGTCCAAAAGTCACTT	2820
Db	2761	AATGTGACAAATCTCTGCCCACTCTCGGGTCTTTAAAGAAACAAAGTCCAAAAGTCACTT	2820
Qy	2821	TTGAACTGTACAAAGGGAAGAAATCAAGGAAGAGATGAGTCTTAATATCAAGCCTGTAC	2880
Db	2821	TTGAACTGTACAAAGGGAAGAAATCAAGGAAGAGATGAGTCTTAATATCAAGCCTGTAC	2880
Qy	2881	AGACAGTTAATATCACTGTGAGGCTTTCTGTGGTTGGTTCAGAAAGATAAGCCAGTTGATA	2940
Db	2881	AGACAGTTAATATCACTGTGAGGCTTTCTGTGGTTGGTTCAGAAAGATAAGCCAGTTGATA	2940
Qy	2941	ATGCCAAATGTAGTATCAAAAGGAGGCTCTAGGTTTTCTCTATCATCTCAGTTCAGAGGCA	3000
Db	2941	ATGCCAAATGTAGTATCAAAAGGAGGCTCTAGGTTTTCTCTATCATCTCAGTTCAGAGGCA	3000

QY	3001	ACGAACTTGGACTCATTTACTCCAAATAAATACATGGACTTTTACAAAACCCATATCGTATAC	3060
DB	3001	ACGAACTTGGACTCATTTACTCCAAATAAATACATGGACTTTTACAAAACCCATATCGTATAC	3060
QY	3061	CACCACTTTTCCCACATCAAGTCAATTTGTTTAAAACTAAATGTAAAGAAAATCTCCTAGAGG	3120
DB	3061	CACCACTTTTCCCACATCAAGTCAATTTGTTTAAAACTAAATGTAAAGAAAATCTCCTAGAGG	3120
QY	3121	AAAACCTTTGAGGAAACATTCATATGTCCCTGAAAGAGAAAATGGGAAAATAGAAACATTTCCAA	3180
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QY	3181	GTACAGTGAAGCAATATAGCCGTAATACATTTAGAGAAAATGTTTTTAAAGAGGCCAGCT	3240
DB	3181	GTACAGTGAAGCAATATAGCCGTAATACATTTAGAGAAAATGTTTTTAAAGAGGCCAGCT	3240
QY	3241	CAAGCAATATTAATGAAGTAGGTTCCAGCTACTAAATGAAGTGGGCTCCAGTATTAAATGAAA	3300
DB	3241	CAAGCAATATTAATGAAGTAGGTTCCAGCTACTAAATGAAGTGGGCTCCAGTATTAAATGAAA	3300
QY	3301	TAGGTTCCAGTGATGAAAACATTCGAGCGAATCTAGGTGAGAAACAGAGGGCCAAAATTGA	3360
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QY	3361	ATGCTATGCTTAGATTAGGGGTTTTGCAACCTGAGGTCTATAAAACAAAGTCTTCTCTGGAA	3420
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DB	3421	GTAATTGTAAGCATCCTGAAATAAAAAAGCAAGAATATGAAGAAGTAGTTCAGACTGTTA	3480
QY	3481	ATACAGATTTCTCTCCATATCTGATTTCCAGATAAATTAGAAACGCTATGGGAAGTAGTC	3540
DB	3481	ATACAGATTTCTCTCCATATCTGATTTCCAGATAAATTAGAAACGCTATGGGAAGTAGTC	3540
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DB	3541	ATGCATCTCAGGTTTGTCTCGAGACACCTGATGACCTGTTAGATGATGGTGAATAAAGG	3600
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DB	3601	AAGATACATAGTTTCTGTAATAATGACATTAAGGAAAGTCTGCTGTTTTTAGCAAAAGCG	3660
QY	3661	TCCAGAGAGGAGAGCTTAGCAGAGTCTCTAGCCCTTTACCCATACACATTTGGCTCAGG	3720
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QY	3721	GTTACCGAAGAGGGGCCAAGAAATTAGAGTCTCTCAGAGAGAACTTATCTAGTGAGGATG	3780
DB	3721	GTTACCGAAGAGGGGCCAAGAAATTAGAGTCTCTCAGAGAGAACTTATCTAGTGAGGATG	3780
QY	3781	AAGAGCTTCCCTGCTTCCAAACATGTTTATTTGGTTAACTAAACATATACCTTCTCAGT	3840
DB	3781	AAGAGCTTCCCTGCTTCCAAACATGTTTATTTGGTTAACTAAACATATACCTTCTCAGT	3840
QY	3841	CTACTAGGCATAGCACCGTTGCTACCGAGTGTCTGCTAAAGAACACAGAGGAGAAATTTAT	3900
DB	3841	CTACTAGGCATAGCACCGTTGCTACCGAGTGTCTGCTAAAGAACACAGAGGAGAAATTTAT	3900
QY	3901	TATCATTTGAAGAAATAGCTTAAATGACTCGAGTAAACAGGTAATATTGGCAAGGCATCTC	3960
DB	3901	TATCATTTGAAGAAATAGCTTAAATGACTCGAGTAAACAGGTAATATTGGCAAGGCATCTC	3960
QY	3961	AGGAACATCACCTTAGTGAGGAAAACAAATGTTCTGCTAGCTGTTTTCTTACAGTGCA	4020
DB	3961	AGGAACATCACCTTAGTGAGGAAAACAAATGTTCTGCTAGCTGTTTTCTTACAGTGCA	4020
QY	4021	GTGAATTTGGAAGACTTGACTGCAAAATACAAACACCCAGGATCCTTTCTTGAATGGTTCCT	4080
DB	4021	GTGAATTTGGAAGACTTGACTGCAAAATACAAACACCCAGGATCCTTTCTTGAATGGTTCCT	4080

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Qy 5701 GCCACTACTGA 5711
Db 5701 GCCACTACTGA 5711

RESULT 12
AR118507 LOCUS AR118507 5712 bp DNA linear PAT 16-MAY-2001
DEFINITION Sequence 1 from patent US 6149903.
ACCESSION AR118507
VERSION AR118507.1 GI:14100417
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 5712)
AUTHORS Holt,J.T., Jensen,R.A., King,M.-C., Page,D.L., Szabo,C.I.,
Jettion,T.L., Robinson-Benion,C.L. and Thompson,M.E.
TITLE Characterized BRCA1 and BRCA2 proteins and screening and
therapeutic methods based on characterized BRCA1 and BRCA2 proteins
JOURNAL Patent: US 6149903-A 1 21-NOV-2000;
FEATURES Location/Qualifiers
source 1..5712
BASE COUNT 1956 a 1099 c 1274 g 1383 t
ORIGIN

Query Match 99.8%; Score 5699.8; DB 6; Length 5712;
Best Local Similarity 99.9%; Pred. No. 0;
Matches 5704; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

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ACCESSION	AR125601	Sequence 1 from patent US 6177410.	linear
VERSION	AR125601.1	GI:14111663	
KEYWORDS			
SOURCE	Unknown.		
ORGANISM	Unknown.		
REFERENCE	Unclassified.		
AUTHORS	1 (bases 1 to 5712)		
TITLE	Holt,J.T., Jensen,R.A., King,M.-C., Steiner,M.S.,		
JOURNAL	Robinson-Benion,C.L. and Thompson,M.E.		
FEATURES	Therapeutic methods for prostate cancer		
	Patent: US 6177410-A 1 23-JAN-2001,		
	Location/Qualifiers		
	1..5712		
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Best Local Similarity 99.8%; Score 5699.8; DB 6; Length 5712;			
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Qy 2521 GTGTGAGTCAAGTGTGAGCAATTTGAAACCCCAAGGACCTAATTTTTCAGAAAG 2580  
Db |||||  
Qy 2521 GTGTGAGTCAAGTGTGAGCAATTTGAAACCCCAAGGACCTAATTTTTCAGAAAG 2580  
Db |||||  
Qy 2581 ATATAGAAATGACAGAGAGGCTTTTAAAGTATCCATTTGGGACATGAAGTTAACCAAGT 2640  
Db |||||  
Qy 2581 ATATAGAAATGACAGAGAGGCTTTTAAAGTATCCATTTGGGACATGAAGTTAACCAAGT 2640  
Db |||||  
Qy 2641 GGGGAAACAGCATAGAAATGGAAGAAAGTGAATTTGATGCTCAGTATTTGAGAAATACAT 2700  
Db |||||  
Qy 2641 GGGGAAACAGCATAGAAATGGAAGAAAGTGAATTTGATGCTCAGTATTTGAGAAATACAT 2700  
Db |||||  
Qy 2701 TCAGGTTTCAAAGCGCCAGTCAATTTGCTCTGTTTTCAGAAATCCAGAAAGG 2760  
Db |||||

Db	2701	TCAGGTTTCAAAGCGCCAGTCATTTGCTCCGTTTTCAAATCCAGGAAATGCAGAAAGG	2760
Qy	2761	AATGTGCACAATTCTCTGCCCACTCTGGGTCCCTTAAAGAAACAAAGTCCAAAAGTCACTT	2820
Db	2761	AATGTGCACAATTCTCTGCCCACTCTGGGTCCCTTAAAGAAACAAAGTCCAAAAGTCACTT	2820
Qy	2821	TTGAATGTGAACAAAAGAGAAANAATCAAGGAAGAATGAGTCTAATATCAAGCCTGTAC	2880
Db	2821	TTGAATGTGAACAAAAGAGAAANAATCAAGGAAGAATGAGTCTAATATCAAGCCTGTAC	2880
Qy	2881	AGACAGTTAATATCATCTGCHAGGCTTTCCTGTGGTTGGTCAAGAAAGATAAGCCAGTTGATA	2940
Db	2881	AGACAGTTAATATCATCTGCHAGGCTTTCCTGTGGTTGGTCAAGAAAGATAAGCCAGTTGATA	2940
Qy	2941	ATGCCAAATGTAGTATCAAAAGGAGGCTCTAGGTTTTGTCATCATCTCAGTTCAGAGGCA	3000
Db	2941	ATGCCAAATGTAGTATCAAAAGGAGGCTCTAGGTTTTGTCATCATCTCAGTTCAGAGGCA	3000
Qy	3001	ACGAAACTGGACCTCATTTACTCCAAATAAAACATGGACTTTTACAAAACCCATATCGTATAC	3060
Db	3001	ACGAAACTGGACCTCATTTACTCCAAATAAAACATGGACTTTTACAAAACCCATATCGTATAC	3060
Qy	3061	CACCACTTTTCCCATCAAGTCATTTGTTAAAACTAAATGTAGAAAAATCTGCTAGAGG	3120
Db	3061	CACCACTTTTCCCATCAAGTCATTTGTTAAAACTAAATGTAGAAAAATCTGCTAGAGG	3120
Qy	3121	AAAACCTTTGAGGAACATTTCAATGTCACCTCAAGAGAGAAATGGGAATGAGAAATTTCCAA	3180
Db	3121	AAAACCTTTGAGGAACATTTCAATGTCACCTCAAGAGAGAAATGGGAATGAGAAATTTCCAA	3180
Qy	3181	GTACAGTGAGCACAAATTTAGCCGTAATAACATTTAGAGAAAAATGTTTTAAAGGAGCCAGCT	3240
Db	3181	GTACAGTGAGCACAAATTTAGCCGTAATAACATTTAGAGAAAAATGTTTTAAAGGAGCCAGCT	3240
Qy	3241	CAAGCAATATTAATGAAGTAGTTTCCAGTACTAATGAAGTGGGCTCCAGTATTAATGAAA	3300
Db	3241	CAAGCAATATTAATGAAGTAGTTTCCAGTACTAATGAAGTGGGCTCCAGTATTAATGAAA	3300
Qy	3301	TAGGTTCCAGTGATGAAAACATTTCAAGCAGACCTAGGTAGAAAACAGAGGGGCCAAAATTGA	3360
Db	3301	TAGGTTCCAGTGATGAAAACATTTCAAGCAGACCTAGGTAGAAAACAGAGGGGCCAAAATTGA	3360
Qy	3361	ATGCTATGCTTAGATTAGGGGTTTTGCAACTGAGGCTATAACAAGTCTTCTCTGGAA	3420
Db	3361	ATGCTATGCTTAGATTAGGGGTTTTGCAACTGAGGCTATAACAAGTCTTCTCTGGAA	3420
Qy	3421	GTAATTGTAGCAATCTTGAAATAAAAAAGCAAGAATATGAAGAAGTAGTTCAGACTGTTA	3480
Db	3421	GTAATTGTAGCAATCTTGAAATAAAAAAGCAAGAATATGAAGAAGTAGTTCAGACTGTTA	3480
Qy	3481	ATACAGATTCTCTCCATATCTGATTTTCAGATAACTTAGAACGCCCTATGGGAAGTAGTC	3540
Db	3481	ATACAGATTCTCTCCATATCTGATTTTCAGATAACTTAGAACGCCCTATGGGAAGTAGTC	3540
Qy	3541	ATGCATCTCAGGTTTTGTTCTGAGACACCTGATGACCTGTTAGATGATGTTGAAATAAAGG	3600
Db	3541	ATGCATCTCAGGTTTTGTTCTGAGACACCTGATGACCTGTTAGATGATGTTGAAATAAAGG	3600
Qy	3601	AAGATACCTAGTTTTGCTGAAATGACATTAAGGAAAGTTCTGCTGTTTTTTAGCAAAAGCG	3660
Db	3601	AAGATACCTAGTTTTGCTGAAATGACATTAAGGAAAGTTCTGCTGTTTTTTAGCAAAAGCG	3660
Qy	3661	TCCAGAGAGGAGACTTAGCGAGAGTCCCTAGCCCTTTTACCCATACATCATTTGGCTCAGG	3720
Db	3661	TCCAGAGAGGAGACTTAGCGAGAGTCCCTAGCCCTTTTACCCATACATCATTTGGCTCAGG	3720
Qy	3721	GTTACCGAAGAGGGGCCAAGAAATTTAGAGTCTCAGAAAGAGAACTTATCTAGTGAAGATG	3780
Db	3721	GTTACCGAAGAGGGGCCAAGAAATTTAGAGTCTCAGAAAGAGAACTTATCTAGTGAAGATG	3780
Qy	3781	AAGAGCTTCCCTGCTTCCACACTTGTATTTTGGTAAAGTAAACAAATATACCTTCTCAGT	3840

3781	Db	AGAGCTTCCTCGTCTCCAAACACCTTGTTATTTGGTAAAGTAACAATATATACCTTCTCTCAGT	3841	Qy	CTACTAGGCATAGCACCGTTTGCTACCGAGTGTCTGTCTAAGAACACAGAGGAGAAATTTAT
3841	Db	CTACTAGGCATAGCACCGTTTGCTACCGAGTGTCTGTCTAAGAACACAGAGGAGAAATTTAT	3901	Qy	TATCATTTGAAGAATAGCTTTAAATGACTGTCAGTAAACAGAGTAAATATTGGCAAAAGGCATCTC
3901	Db	TATCATTTGAAGAATAGCTTTAAATGACTGTCAGTAAACAGAGTAAATATTGGCAAAAGGCATCTC	3961	Qy	AGGAACATCACCTTAGTGAGGAACAATAATGTTCTCTGCTAGCTTGTCTTCTTCAACAGTGCA
3961	Db	AGGAACATCACCTTAGTGAGGAACAATAATGTTCTCTGCTAGCTTGTCTTCTTCAACAGTGCA	4021	Qy	GTGAATTTGGAAGACTTGACTGCAAATACAAACACCCAGGATCCCTTTCTTGATTTGGTTCTTT
4021	Db	GTGAATTTGGAAGACTTGACTGCAAATACAAACACCCAGGATCCCTTTCTTGATTTGGTTCTTT	4081	Qy	CCAAACAAATGAGGCATCAGTCTGAAAGCCAGGGAGTTGGTCTGAGTGACAAGGAATTTGG
4081	Db	CCAAACAAATGAGGCATCAGTCTGAAAGCCAGGGAGTTGGTCTGAGTGACAAGGAATTTGG	4141	Qy	TTTTCAGATGATGAAGAAGAGGAACGGCTTGGAAGAAATAATCAAGRAGACRAAGCA
4141	Db	TTTTCAGATGATGAAGAAGAGGAACGGCTTGGAAGAAATAATCAAGRAGACRAAGCA	4201	Qy	TGGATTCAAACTTTAGGTGAAGCAGCATCTCGGTGTGAGAGTGAAAAACAGCGTCTCTGGAAG
4201	Db	TGGATTCAAACTTTAGGTGAAGCAGCATCTCGGTGTGAGAGTGAAAAACAGCGTCTCTGGAAG	4261	Qy	ACTGCTCAGGGCTATCCTCTCAGAGTGACATTTTAAACCCTCAGCAGAGGGATACCAATGC
4261	Db	ACTGCTCAGGGCTATCCTCTCAGAGTGACATTTTAAACCCTCAGCAGAGGGATACCAATGC	4321	Qy	AACATAACCTGATTAAGCTCCAGCAGGAATGCGTGNAACTAGAGCTGTGTGTAGAACAGC
4321	Db	AACATAACCTGATTAAGCTCCAGCAGGAATGCGTGNAACTAGAGCTGTGTGTAGAACAGC	4381	Qy	ATGGAGCCAGCCCTTCTFAACAGCTACCCCTTCCATCATAACTGACTCTCTCGCCCTTGAGG
4381	Db	ATGGAGCCAGCCCTTCTFAACAGCTACCCCTTCCATCATAACTGACTCTCTCGCCCTTGAGG	4441	Qy	ACCTTGGGAATCCAGAACAAAGCACATCAGAAAAAGCAGTATTAACTTCACAGAAAAAGTA
4441	Db	ACCTTGGGAATCCAGAACAAAGCACATCAGAAAAAGCAGTATTAACTTCACAGAAAAAGTA	4501	Qy	GTGAATACCCCTATTAAGCCAGAAATCCAGAGCCCTTTCTGCTGACAAGTTTGAAGTGTCTG
4501	Db	GTGAATACCCCTATTAAGCCAGAAATCCAGAGCCCTTTCTGCTGACAAGTTTGAAGTGTCTG	4561	Qy	CAGATAGTCTTACCAGTAAAAATAAGAAACAGAGGTGAAAGGTCAATCCCTTCTTAAAT
4561	Db	CAGATAGTCTTACCAGTAAAAATAAGAAACAGAGGTGAAAGGTCAATCCCTTCTTAAAT	4621	Qy	GCCCATCATTTAGATGATAGTGGTGTACATGCACAGTTGCTCTCGGAGTCTTTCAGAATAGAA
4621	Db	GCCCATCATTTAGATGATAGTGGTGTACATGCACAGTTGCTCTCGGAGTCTTTCAGAATAGAA	4681	Qy	ACTAACCATCTCAAGAGGAGCTCATTAAGGTTGTTGATGTGGAGGAGCAACAGCTGGAAG
4681	Db	ACTAACCATCTCAAGAGGAGCTCATTAAGGTTGTTGATGTGGAGGAGCAACAGCTGGAAG	4741	Qy	AGTCTGGGGCCACAGATTTGACGGAAACATCTTACATTTGCCAAGCAAGATCTAGAGGGAA
4741	Db	AGTCTGGGGCCACAGATTTGACGGAAACATCTTACATTTGCCAAGCAAGATCTAGAGGGAA	4801	Qy	CCCCCTTACCTGGAACTCTGGAAATCAGCCCTCTTCTCTGTATGATCCCTTGAATCTGATCTCTG
4801	Db	CCCCCTTACCTGGAACTCTGGAAATCAGCCCTCTTCTCTGTATGATCCCTTGAATCTGATCTCTG	4861	Qy	AAGACAGAGCCCGAGTGTGCTGTTGGCAACATACCATCTTCAACCTCTGCATTTGA
4861	Db	AAGACAGAGCCCGAGTGTGCTGTTGGCAACATACCATCTTCAACCTCTGCATTTGA	4921	Qy	AGAGCAGAGCCCGAGTGTGCTGTTGGCAACATACCATCTTCAACCTCTGCATTTGA





Qy 961 GCTCATTACAGCATGAGAACAGCAGTGTATTTACTCACTAAAGACAGAGTGAATGTAGAAA 1020  
Db 961 GCTCATTACAGCATGAGAACAGCAGTGTATTTACTCACTAAAGACAGAGTGAATGTAGAAA 1020  
Qy 1021 AGGCTGAATCTGTAAATAAAGCAAAACAGCCTGGCTTAGCAAGGAGCCAAACATACAGAT 1080  
Db 1021 AGGCTGAATCTGTAAATAAAGCAAAACAGCCTGGCTTAGCAAGGAGCCAAACATACAGAT 1080  
Qy 1081 GGGCTGAGAGTAAGGAAACATGTATGATAGGCGGACTCCAGACAGAGAAAAAGGTAG 1140  
Db 1081 GGGCTGAGAGTAAGGAAACATGTATGATAGGCGGACTCCAGACAGAGAAAAAGGTAG 1140  
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GenCore version 5.1.6  
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Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	5711	100.0	5711	18	Human BRCA1 gene c
2	5711	100.0	5711	19	BRCA1 (omil) codin
3	5711	100.0	5711	19	Human BRCA1 omil c
4	5711	100.0	5711	21	Human BRCA1 (omil)
5	5710.6	100.0	5711	19	Human BRCA1 omil3 p
6	5710.6	100.0	5711	19	Human BRCA1 omil p
7	5710.6	100.0	5711	19	Human BRCA1 omil p
8	5710.6	100.0	5711	19	Human BRCA1 omil p

9	5710.6	100.0	5711	19	AAV46454	Human BRCA1 omil p
10	5710.6	100.0	5711	19	AAV46455	Human BRCA1 omil p
11	5710.6	100.0	5711	19	AAV46456	Human BRCA1 omil p
12	5710.6	100.0	5711	19	AAV46457	Human BRCA1 omil p
13	5709.4	100.0	5711	19	AAV46450	Human BRCA1 omil3 c
14	5709.4	100.0	5711	21	AAC60794	Human BRCA1 (omil2)
15	5709	100.0	5711	19	AAV46455	Human BRCA1 omil3 p
16	5709	100.0	5711	19	AAV46456	Human BRCA1 omil3 p
17	5709	100.0	5711	19	AAV46457	Human BRCA1 omil3 p
18	5709	100.0	5711	19	AAV46458	Human BRCA1 omil3 p
19	5709	100.0	5711	19	AAV46459	Human BRCA1 omil3 p
20	5709	100.0	5711	19	AAV46460	Human BRCA1 omil3 p
21	5702.6	99.9	5711	19	AAV46461	Human BRCA1 omil2 p
22	5702.6	99.9	5711	19	AAV46462	Human BRCA1 omil2 p
23	5702.6	99.9	5711	19	AAV46463	Human BRCA1 omil2 p
24	5702.6	99.9	5711	19	AAV46464	Human BRCA1 omil2 p
25	5702.6	99.9	5711	19	AAV46465	Human BRCA1 omil2 p
26	5701.4	99.8	5711	19	AAV46466	Human BRCA1 omil2 c
27	5701.4	99.8	5711	21	AAC60795	Human BRCA1 (omil3)
28	5701.4	99.8	5711	17	AAT17491	Mutated BRCA1 codi
29	5701.4	99.8	5711	17	AAT17492	Mutated BRCA1 codi
30	5701.4	99.8	5711	17	AAT17493	Mutated BRCA1 codi
31	5701.4	99.8	5711	17	AAT17494	Mutated BRCA1 codi
32	5701.4	99.8	5711	17	AAT17495	Mutated BRCA1 codi
33	5701.4	99.8	5711	17	AAT17496	Mutated BRCA1 codi
34	5701	99.8	5711	19	AAV46458	Human BRCA1 omil2 p
35	5701	99.8	5711	25	AB223502	Nucleotide sequenc
36	5699.8	99.8	5711	18	AAT84840	Human breast and o
37	5699.8	99.8	5712	18	AAT84840	BRCA1 gene sequenc
38	5699.8	99.8	5712	21	AAT87995	BRCA1, breast and
39	5699.8	99.8	5714	17	AAT12601	BRCA1 coding sequ
40	5699.8	99.8	5714	17	AAT17438	BRCA1, breast and
41	5699.8	99.8	5714	17	AAT18310	BRCA1, breast and
42	5698.2	99.8	5711	17	AAT42024	BRCA1 allele #8403
43	5698.2	99.8	5711	17	AAT42030	BRCA1 allele #7408
44	5698.2	99.8	5711	18	AAT70067	Mutant BRCA1 allel
45	5698.2	99.8	5711	18	AAT70073	Mutant BRCA1 allel

#### ALIGNMENTS

RESULT 1  
AAT87085  
ID AAT87085 standard; cDNA; 5711 BP.  
XX  
AC AAT87085;  
XX  
DT 06-JAN-1998 (first entry)  
XX  
DB Human BRCA1 gene consensus.  
XX  
KW BRCA1 gene; BRCA1(omil); breast cancer; ovary cancer; polymorphism;  
KW genetic testing; diagnosis; gene therapy; ss.  
XX  
OS Homo sapiens.  
XX  
FH Key Location/Qualifiers  
FT CDS 120..5711  
FT FT /\*tag= a  
FT FT 2201  
FT FT /\*tag= b  
FT FT /\*note= "AGC (40%) and AGT (55-65%) polymorphism  
FT FT at position 2201"  
FT FT 2430  
FT FT /\*tag= c  
FT FT /\*note= "35-45% TTG (leu) and 55-65% CTG (Leu)  
FT FT polymorphism at position 2430"  
FT FT 2731  
FT FT /\*tag= d  
FT FT /\*note= "25-35% CCG (Pro) and 65-75% CTG (Leu)  
FT FT polymorphism at position 2731"  
FT FT 3232



Qy	1321	GGGAGTCTGAATCAATGCCAAGTAGCTGATGATTTGGAGCGTTCTAAATGAGGTAGATG	1380
Db	1321		
Qy	1381	GGGAGTCTGAATCAAAATGCCAAGTAGCTGATGATTTGGAGCGTTCTAAATGAGGTAGATG	1380
Db	1381		
Qy	1441	AATATTCTGGTTCTTCAGAGAAATAGACTTACTGGCCAGTGATCCTCATGAGCGCTTTAA	1440
Db	1441		
Qy	1441	AATATTCTGGTTCTTCAGAGAAATAGACTTACTGGCCAGTGATCCTCATGAGCGCTTTAA	1440
Db	1441		
Qy	1501	TATGTAAAGTGAAGAGTTCACCTCCAAATCAGTAGAGAGTAATATTGAAGACAAATAT	1500
Db	1501		
Qy	1501	TTGGGAAAACCTTATCGGAAGAGCGCAAGCCTCCCAATCTTAAGCCATGTAACTGAAATC	1560
Db	1501		
Qy	1561	TAATTATPAGGAGCATTTGTACTGAGCCACAGATAATACAGAGCGTCCCTCCACAATA	1620
Db	1561		
Qy	1621	AATTTAAAGCGTAAAGGAGACCTACATCAGGCGCTTCATCTGAGGATTTTATCAAGAAAG	1680
Db	1621		
Qy	1681	CAGATTTGGCAGTTCAAAAGACTCCTGAAATGATAAATCAGGGAATTAACCAACGGAGC	1740
Db	1681		
Qy	1741	AGATGTCAGTGATGAATTAATTAATAGTGTGTCATGAGATATAAACAAGAGTGATT	1800
Db	1741		
Qy	1801	CTATTCAAGATGAGAAATCTTAACCAATAGAAATCACTCGAATAAGAAATCTGCTTTCA	1860
Db	1801		
Qy	1861	AAACGAAAGCTGAACTTAAAGCAGCAGTATAAGCAATATGGAATCGAAATTAATAATCC	1920
Db	1861		
Qy	1921	ACAAATCAAAAGCCTTAAAGAAATAGGCTGAGGAGGAAGTCTTTACACAGGCATATTC	1980
Db	1921		
Qy	1981	ATGCGCTTGAACCTTAAAGAAATAGGCTGAGGAGGAAGTCTTTACACAGGCATATTC	2040
Db	1981		
Qy	2041	TTGATAGTTGTTCTPAGCAGTGAAGAGATAAGAAAAAAGTACAAACCAATGCCAGTCA	2100
Db	2041		
Qy	2101	GGCAGCAGAAACCTTCAACTATGGAAGTAAAGAACTTGCACTGGAGCCAAAGA	2160
Db	2101		
Qy	2161	GTCACAGCAGAAACCTTCAACTATGGAAGTAAAGAACTTGCACTGGAGCCAAAGA	2220
Db	2161		
Qy	2221	AGTTAAACAAATGCAACCTTCTTTTACTAGTGTCCAAATACCAGTGAACCTTAAGAAT	2280
Db	2221		
Qy	2281	TTGTCAAATCTAGCCTTCCAAAGAGAAAGAGAGAACTAGAAAACAGTTAAAGTGT	2340
Db	2281		
Qy	2341	CTAATAATGCTGAAGACCCCAAGATCTCATGTTAAGTGGAGAAAGGGTTTGCAAACTG	2400
Db	2341		
Qy	2401	AAAGATCTGTAGAGTAGCAGTATTTTCACTGCTACTGCTACTGATTTATGGCACTCAGG	2460
Db	2401		
Qy	2461	AAAGATCTGTAGAGTAGCAGTATTTTCACTGCTACTGCTACTGATTTATGGCACTCAGG	2460
Db	2461		
Qy	2521	GTGTAGTCACTGTGAGCAATTTGAAACCCCAAGGCACTAAATTCATGGTGTGTTCCAAAG	2580
Db	2521		
Qy	2581	ATTAATAGAAATGACACAGAAGGCTTTAAAGTATCCATTTGGGACATGAAGTTAACACAGTC	2640
Db	2581		
Qy	2641	GGGAAACCAAGCATAGAAATGGAAGAGTGAATTTGATGCTCAGTATTTGCGAGAAATACAT	2700
Db	2641		
Qy	2701	TCAAGGTTTCAAAGCGCCAGTCAATTTGCTCTGTTTTCAAAATCCAGGAAATGCGAGAAGG	2760
Db	2701		
Qy	2761	AATGTGCAACATTTCTGTGCCCCACTCTGGGCTCTTAAAGAAACAAAGTCCAAAAGTCACTT	2820
Db	2761		
Qy	2821	TTGAATGTGAACAAAGGAGAGAAATCAAGGAAAGATGAGTCTAAATCAAGGCTGTAC	2880
Db	2821		
Qy	2881	AGACAGTTAATATACATCGCAGGCTTTCTCTGTTGCTCAGAAAGATAAGCCAGTTGATA	2940
Db	2881		
Qy	2941	ATGCCAAATGTAGTATCAAAAGGAGGCTCTAGGTTTCTCTATCATCTCAGTTTCAGAGCA	3000
Db	2941		
Qy	3001	ACGAAATGCACTCATTTACTCCAAATAAATGAGGCTTTTACAAAACCCATATCGTATAC	3060
Db	3001		
Qy	3061	CACCACTTTTCCCATCAAGTCAATTTCTTAAACTAAATGTAAAGAAATCTGCTAGAGG	3120
Db	3061		
Qy	3121	AAAACTTTGAGGAACATTTCAATGTCACTGAAAGAGAAATGGGAAATGAGAAATTCCTAA	3180
Db	3121		
Qy	3181	GTACAGTGACCAATTTAGCCGTAATTAACATTAGAGAAATGTTTTTAAAGGAGCCAGCT	3240
Db	3181		
Qy	3241	CAAGCAATTAATTAAGTAGGTTTCCAGTACTAATGAAGTGGGCTCCAGTATTAATGAAA	3300
Db	3241		
Qy	3301	TAGGTTCCAGTGATGAAAACATTTCAAGCAGAACTAGGTAGAAAACAGAGGGCCAAATTTGA	3360
Db	3301		
Qy	3361	ATGCTATGCTTAGATTAGGGGTTTTGCAACTGAGGCTCTATAAACAAGTCTTCTCTGAA	3420
Db	3361		
Qy	3421	GTAAATGTAGCATCTCGAAATAAAGCAAGNATATGAGAGTATTGAGACTGTTA	3480
Db	3421		
Qy	3481	ATACAGATTTCTCTCCATATCTGATTTTCAATTAACAGCCTATGGGAAGTAGTC	3540
Db	3481		

Qy	2401	AAAGATCTGTAGAGTAGCAGTATTTTCACTGCTACTGCTACTGATTTATGGCACTCAGG	2460
Db	2401		
Qy	2461	AAAGATCTGTAGAGTAGCAGTATTTTCACTGCTACTGCTACTGATTTATGGCACTCAGG	2460
Db	2461		
Qy	2521	GTGTAGTCACTGTGAGCAATTTGAAACCCCAAGGCACTAAATTCATGGTGTGTTCCAAAG	2580
Db	2521		
Qy	2581	ATTAATAGAAATGACACAGAAGGCTTTAAAGTATCCATTTGGGACATGAAGTTAACACAGTC	2640
Db	2581		
Qy	2641	GGGAAACCAAGCATAGAAATGGAAGAGTGAATTTGATGCTCAGTATTTGCGAGAAATACAT	2700
Db	2641		
Qy	2701	TCAAGGTTTCAAAGCGCCAGTCAATTTGCTCTGTTTTCAAAATCCAGGAAATGCGAGAAGG	2760
Db	2701		
Qy	2761	AATGTGCAACATTTCTGTGCCCCACTCTGGGCTCTTAAAGAAACAAAGTCCAAAAGTCACTT	2820
Db	2761		
Qy	2821	TTGAATGTGAACAAAGGAGAGAAATCAAGGAAAGATGAGTCTAAATCAAGGCTGTAC	2880
Db	2821		
Qy	2881	AGACAGTTAATATACATCGCAGGCTTTCTCTGTTGCTCAGAAAGATAAGCCAGTTGATA	2940
Db	2881		
Qy	2941	ATGCCAAATGTAGTATCAAAAGGAGGCTCTAGGTTTCTCTATCATCTCAGTTTCAGAGCA	3000
Db	2941		
Qy	3001	ACGAAATGCACTCATTTACTCCAAATAAATGAGGCTTTTACAAAACCCATATCGTATAC	3060
Db	3001		
Qy	3061	CACCACTTTTCCCATCAAGTCAATTTCTTAAACTAAATGTAAAGAAATCTGCTAGAGG	3120
Db	3061		
Qy	3121	AAAACTTTGAGGAACATTTCAATGTCACTGAAAGAGAAATGGGAAATGAGAAATTCCTAA	3180
Db	3121		
Qy	3181	GTACAGTGACCAATTTAGCCGTAATTAACATTAGAGAAATGTTTTTAAAGGAGCCAGCT	3240
Db	3181		
Qy	3241	CAAGCAATTAATTAAGTAGGTTTCCAGTACTAATGAAGTGGGCTCCAGTATTAATGAAA	3300
Db	3241		
Qy	3301	TAGGTTCCAGTGATGAAAACATTTCAAGCAGAACTAGGTAGAAAACAGAGGGCCAAATTTGA	3360
Db	3301		
Qy	3361	ATGCTATGCTTAGATTAGGGGTTTTGCAACTGAGGCTCTATAAACAAGTCTTCTCTGAA	3420
Db	3361		
Qy	3421	GTAAATGTAGCATCTCGAAATAAAGCAAGNATATGAGAGTATTGAGACTGTTA	3480
Db	3421		
Qy	3481	ATACAGATTTCTCTCCATATCTGATTTTCAATTAACAGCCTATGGGAAGTAGTC	3540
Db	3481		

Db	3481		ATACAGAA	TTCTCT	CCCATAT	CTGATTT	CAGATAA	CTTTAGAAC	CCCTAT	TGGGAAG	TAGTC	3540							
Qy	3541	ATGCAT	CTCAGG	TTTGTT	CTTGAGAC	ACCTGAT	GACCTG	TTAGATG	ATGATG	GTGGT	GAAATAA	AGG	3600						
Db	3541	ATGCAT	CTCAGG	TTTGTT	CTTGAGAC	ACCTGAT	GACCTG	TTAGATG	ATGATG	GTGGT	GAAATAA	AGG	3600						
Qy	3601	AAGAT	TACTAG	TTTTGCT	GAAAA	TGACAT	TAAAG	AAAGTT	CTGCTG	TTTTTTAG	CAAAAGCG	3660							
Db	3601	AAGAT	TACTAG	TTTTGCT	GAAAA	TGACAT	TAAAG	AAAGTT	CTGCTG	TTTTTTAG	CAAAAGCG	3660							
Qy	3661	TCCAGAG	AGGAGC	TTAGCAG	GGAGT	CCTAG	CCCTTT	CACCC	ATACAC	ATTGCG	CTCAGG	3720							
Db	3661	TCCAGAG	AGGAGC	TTAGCAG	GGAGT	CCTAG	CCCTTT	CACCC	ATACAC	ATTGCG	CTCAGG	3720							
Qy	3721	GTTAC	CGAAG	GGGGCC	AAGAA	TTAGAG	TCCTC	AGAG	AAGAA	CTTAT	CTAGT	GAGATG	3780						
Db	3721	GTTAC	CGAAG	GGGGCC	AAGAA	TTAGAG	TCCTC	AGAG	AAGAA	CTTAT	CTAGT	GAGATG	3780						
Qy	3781	AAGAG	CTTCC	CTGCTT	CCAA	CAC	TGTTAT	TTGGT	AAAGT	AAACAA	TATAT	ACCTT	CTCAGT	3840					
Db	3781	AAGAG	CTTCC	CTGCTT	CCAA	CAC	TGTTAT	TTGGT	AAAGT	AAACAA	TATAT	ACCTT	CTCAGT	3840					
Qy	3841	CTA	CTAGG	CATAG	CAC	CGTTG	CTAC	CGAGT	GTCTGT	CTAA	GAAACAC	AGAGG	AAATTTAT	3900					
Db	3841	CTA	CTAGG	CATAG	CAC	CGTTG	CTAC	CGAGT	GTCTGT	CTAA	GAAACAC	AGAGG	AAATTTAT	3900					
Qy	3901	TATCA	TTGA	AGNAT	TAGCT	TAAAT	GAC	TCGAGT	AAACAG	GTAAT	TTGGC	AAAGGC	ATCTC	3960					
Db	3901	TATCA	TTGA	AGNAT	TAGCT	TAAAT	GAC	TCGAGT	AAACAG	GTAAT	TTGGC	AAAGGC	ATCTC	3960					
Qy	3961	AGGAA	CATCAC	CTT	PAGT	GAGG	AAACAAA	ATGTT	CTGCTAG	CTTGT	TTTCTT	CACAGT	GC	4020					
Db	3961	AGGAA	CATCAC	CTT	PAGT	GAGG	AAACAAA	ATGTT	CTGCTAG	CTTGT	TTTCTT	CACAGT	GC	4020					
Qy	4021	GTGA	ATTTGG	AAAGCT	TGAC	TGC	AAATA	CAAA	ACCCAG	AGTCC	TTTCTT	GATTTGG	TTCTT	4080					
Db	4021	GTGA	ATTTGG	AAAGCT	TGAC	TGC	AAATA	CAAA	ACCCAG	AGTCC	TTTCTT	GATTTGG	TTCTT	4080					
Qy	4081	CCAA	CAAA	TGAG	GCAT	CAGT	CTG	TAAAG	CCAGG	AGTTGGT	CTGAGT	GAC	AGGAAT	TGG	4140				
Db	4081	CCAA	CAAA	TGAG	GCAT	CAGT	CTG	TAAAG	CCAGG	AGTTGGT	CTGAGT	GAC	AGGAAT	TGG	4140				
Qy	4141	TTT	CAGAT	GATGA	AAAG	AGG	AAACGG	GGCTT	TGGA	AGAAA	ATAAT	CAAGA	AGAC	CAAGCA	4200				
Db	4141	TTT	CAGAT	GATGA	AAAG	AGG	AAACGG	GGCTT	TGGA	AGAAA	ATAAT	CAAGA	AGAC	CAAGCA	4200				
Qy	4201	TGGAT	TCAA	ACTTTAG	TGTA	AGCAG	CATCT	GGGTG	TGAG	AGTGA	AAACAG	CGTCT	CTCAAG	4260					
Db	4201	TGGAT	TCAA	ACTTTAG	TGTA	AGCAG	CATCT	GGGTG	TGAG	AGTGA	AAACAG	CGTCT	CTCAAG	4260					
Qy	4261	ACTG	CTCAGG	GCAT	CTCT	CAGAGT	GACAT	TTTAA	CCATC	AGAGGGAT	TACCAT	GC	4320						
Db	4261	ACTG	CTCAGG	GCAT	CTCT	CAGAGT	GACAT	TTTAA	CCATC	AGAGGGAT	TACCAT	GC	4320						
Qy	4321	AAC	TAACT	CTGATA	AAAG	CTC	CAG	AGAA	ATGG	CTGAA	CTTAG	AGAGT	GTCT	TAGAAC	AGC	4380			
Db	4321	AAC	TAACT	CTGATA	AAAG	CTC	CAG	AGAA	ATGG	CTGAA	CTTAG	AGAGT	GTCT	TAGAAC	AGC	4380			
Qy	4381	ATGG	AGCC	AGC	CTTCT	TAA	CAG	CTTAC	CCCTT	CCAT	CTA	TAA	AGT	GACT	CTCT	CTG	CCCTT	GAGG	4440
Db	4381	ATGG	AGCC	AGC	CTTCT	TAA	CAG	CTTAC	CCCTT	CCAT	CTA	TAA	AGT	GACT	CTCT	CTG	CCCTT	GAGG	4440
Qy	4441	AC	TGCG	AAAT	CCAG	AA	CAAG	CACAT	CAGAAA	AGCAG	TATTA	ACTT	CAC	AGAA	AGTA	4500			
Db	4441	AC	TGCG	AAAT	CCAG	AA	CAAG	CACAT	CAGAAA	AGCAG	TATTA	ACTT	CAC	AGAA	AGTA	4500			
Qy	4501	GTGA	A	TACC	CTTAT	AA	GCAG	AA	TCCAG	AGG	CCCTTT	CTG	CTG	TGA	CAAG	TTT	TGAG	GTCTG	456

Qy 5701 GCCACTACTGA 5711  
 Db 5701 GCCACTACTGA 5711

RESULT 2  
 AAV62180  
 ID AAV62180 standard; DNA; 5711 BP.  
 XX  
 AC AAV62180;  
 XX  
 DT 11-FEB-1999 (first entry)  
 XX  
 DE BRCA1 (om1) coding sequence.  
 XX  
 KW BRCA1; mutation detection; disease screening; multiple allele variation;  
 KW breast cancer; ovarian cancer; cystic fibrosis; Li-Fraumeni syndrome;  
 KW Duchenne muscular dystrophy; Becker muscular dystrophy; ss.  
 XX  
 OS Homo sapiens.  
 XX  
 FH Key Location/Qualifiers  
 FT CDS 120..5711  
 FT /\*tag= a  
 XX  
 XX WO9844157-A2.  
 XX  
 XX 08-OCT-1998.  
 XX  
 XX 26-MAR-1998; 98WO-US06002.  
 XX  
 XX 28-MAR-1997; 97US-0825487.  
 XX  
 XX (ONCO-) ONCORMED INC.  
 XX  
 XX Murphy PD, White MB;  
 XX  
 XX WPI; 1998-542713/46.  
 XX  
 XX P-PSDB; AAW79665.  
 XX

Identifying variations in polynucleotide sequences - using allele  
 specific hybridisation assay, sequence variation locating assay, and  
 direct sequencing, in a stepwise procedure

Disclosure; Fig 1a-j; 62pp; English.

This sequence encodes the human BRCA (om1) protein, and was used to test  
 the method of the invention. The method is for determining the presence  
 or absence of a sequence variation in a gene sample, and comprises:  
 (a) performing an allele specific hybridisation assay for one or more  
 pre-determined sequence variations; (b) if no pre-determined sequence  
 variation found in step (a) then performing a sequence variation location  
 assay; (ci) if no sequence variation found in step (b) then sequencing  
 the gene sample; (cii) if sequence variation is found in step (b) then  
 targeted confirmatory sequencing is performed; and (d) determining the  
 presence of a sequence variation by analysing the sequence(s) obtained in  
 step (ci) or step (cii) against a reference sample. Alternatively, step  
 (a) or step (b) is omitted from the method. The invention provides a  
 stepwise and integrated method for the efficient and accurate detection  
 of variations in polynucleotide sequences, being directed towards  
 screening for diseases associated with multiple allele variations,  
 including breast and ovarian cancer, cystic fibrosis, Duchenne and Becker  
 muscular dystrophy, and Li-Fraumeni syndrome.

Sequence 5711 BP; 1953 A; 1099 C; 1277 G; 1382 T; 0 other;

Query Match 100.0%; Score 5711; DB 19; Length 5711;  
 Best Local Similarity 100.0%; Pred. No. 0;  
 Matches 5711; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

1 AGCTCGCTGAGACTTCTCGGACCCCGCACAGGCTGTGGGGTTTCTCAGATAACTGGGCC 60  
 61 CTTGCGCTCAGGAGGCTTCAACCTCTGCTCTGGTAAAGTTTATTGGAAACAGAAAGAAA 120  
 61 CTTGCGCTCAGGAGGCTTCAACCTCTGCTCTGGTAAAGTTTATTGGAAACAGAAAGAAA 120  
 121 TGGATTATCTGCTCTCTCGGCTTGAAGAAGTACAAAATGTCATTAAATGCTATGAGAAA 180  
 121 TGGATTATCTGCTCTCTCGGCTTGAAGAAGTACAAAATGTCATTAAATGCTATGAGAAA 180  
 181 TCTTAGAGTGTCCATCTGCTGAGTGTGATCAAGGAACCTGTCTCAACAAGTGTGACC 240  
 181 TCTTAGAGTGTCCATCTGCTGAGTGTGATCAAGGAACCTGTCTCAACAAGTGTGACC 240  
 241 ACATATTTTGCATAATTTTGCATGCTGAAACTTCTCAACAGAAAGAGGCTTTCACAGT 300  
 241 ACATATTTTGCATAATTTTGCATGCTGAAACTTCTCAACAGAAAGAGGCTTTCACAGT 300  
 301 GTCTTTTATGTAAGATGATATACCAAAAGAGGCTTACAAAGAAAGTACGAGATTAGTC 360  
 301 GTCTTTTATGTAAGATGATATACCAAAAGAGGCTTACAAAGAAAGTACGAGATTAGTC 360  
 361 AACTTGTGGAAGAGCTATTGAAATCATTTGTGCTTTTTCAGCTTGACACAGGTTTGGAGT 420  
 361 AACTTGTGGAAGAGCTATTGAAATCATTTGTGCTTTTTCAGCTTGACACAGGTTTGGAGT 420  
 421 ATGCAACAGCTATATATTTTGCATAAAAGGAAATAACTCTCTGGAACATCTAAAGATG 480  
 421 ATGCAACAGCTATATATTTTGCATAAAAGGAAATAACTCTCTGGAACATCTAAAGATG 480  
 481 AAGTTTCTATCTCAAAAGTATGGGCTACAGAAACCGTGCACAAAGACTTCTACAGAGTG 540  
 481 AAGTTTCTATCTCAAAAGTATGGGCTACAGAAACCGTGCACAAAGACTTCTACAGAGTG 540  
 541 AACCCGAAATCTCTTCTCGAGGAAACCAAGTCTCAGTGTCCAATCTCTAACCTTGGAA 600  
 541 AACCCGAAATCTCTTCTCGAGGAAACCAAGTCTCAGTGTCCAATCTCTAACCTTGGAA 600  
 601 CTGTGAGAACTCTGAGGACAAAGCAGCGGATACAACTCAAAAGACGCTCTCTACATTTG 660  
 601 CTGTGAGAACTCTGAGGACAAAGCAGCGGATACAACTCAAAAGACGCTCTCTACATTTG 660  
 661 AATTGGGATCTGATTTCTTCAAGATACCGTTAATAAGGCAACTTATTTGCAAGTGTGGAG 720  
 661 AATTGGGATCTGATTTCTTCAAGATACCGTTAATAAGGCAACTTATTTGCAAGTGTGGAG 720  
 721 ATCAAGAAATTTTACAATCAACCTCAAGAACCCAGGATGAAATCAGTTTGGATTCTG 780  
 721 ATCAAGAAATTTTACAATCAACCTCAAGAACCCAGGATGAAATCAGTTTGGATTCTG 780  
 781 CAAAAAGGCTGCTTGTGAATTTTCTGAGCGGATGTAAACAAATCTGAAACATCATCAAC 840  
 781 CAAAAAGGCTGCTTGTGAATTTTCTGAGCGGATGTAAACAAATCTGAAACATCATCAAC 840  
 841 CCAGTAATAATGATTTGAAACACCACTGAGAAGCGTGCAGCTGAGAGGCATCCAGAAAAGT 900  
 841 CCAGTAATAATGATTTGAAACACCACTGAGAAGCGTGCAGCTGAGAGGCATCCAGAAAAGT 900  
 901 ATCAGGAGTGTCTGTTTCAAACTTGCATGTGAGGACCATGTGGCACAATACTCATGCCA 960  
 901 ATCAGGAGTGTCTGTTTCAAACTTGCATGTGAGGACCATGTGGCACAATACTCATGCCA 960  
 961 GCTCATTTACAGCATGAGAACAGCAGTTTATTACTCACTTAAGACAGATGAATGTAGAAA 1020  
 961 GCTCATTTACAGCATGAGAACAGCAGTTTATTACTCACTTAAGACAGATGAATGTAGAAA 1020  
 1021 AGGCTGAATTTCTGTAATAAAAGCAACAGCTGCTGTAGCAAGGAGCCAAATACAGAT 1080  
 1021 AGGCTGAATTTCTGTAATAAAAGCAACAGCTGCTGTAGCAAGGAGCCAAATACAGAT 1080  
 1081 GGGCTGGAAGTAAAGAAACATGTAAATGATAGGCGGACTCCACGACACAGAAAAGGTAG 1140  
 1081 GGGCTGGAAGTAAAGAAACATGTAAATGATAGGCGGACTCCACGACACAGAAAAGGTAG 1140





Db	3301	TAGGTTCCAGTGATGAAACCAATTCACGCGAACTTAGGTAGAAAACAGAGGCGCCAAAATTGA 3360
Qy	3361	ATGCTATGCTTAGATTAGGGGTTTGCAAAGCTGAGGCTTATAAACAAAGTCTTCTCTGGAA 3420
Db	3361	ATGCTATGCTTAGATTAGGGGTTTGCAAAGCTGAGGCTTATAAACAAAGTCTTCTCTGGAA 3420
Qy	3421	GTAATTGTAAAGCATCTGGAATAAAAAAGCAAGATATGAAGAAGTAGTTCAGACGTGTTA 3480
Db	3421	GTAATTGTAAAGCATCTGGAATAAAAAAGCAAGATATGAAGAAGTAGTTCAGACGTGTTA 3480
Qy	3481	ATACAGATTCTCTCCATATCTGATTTTCAGATTAACCTTAGAACGCTTATGGGAAGTAGTC 3540
Db	3481	ATACAGATTCTCTCCATATCTGATTTTCAGATTAACCTTAGAACGCTTATGGGAAGTAGTC 3540
Qy	3541	ATGCATCTCAGGTTTGTTCTTGAGACACCTGATGACCTGTTAGATGATGGTGAATAAAGG 3600
Db	3541	ATGCATCTCAGGTTTGTTCTTGAGACACCTGATGACCTGTTAGATGATGGTGAATAAAGG 3600
Qy	3601	AAGATACTAGTTTGTCTGAAATAGACATTAAGGAAGTTCTGCTGTTTTTGTAGCAAAAGCG 3660
Db	3601	AAGATACTAGTTTGTCTGAAATAGACATTAAGGAAGTTCTGCTGTTTTTGTAGCAAAAGCG 3660
Qy	3661	TCCAGAGAGGAGCCTTAGCAGGAGTCCCTAGCCCTTTCACCCATACACATTTGGCTCAGG 3720
Db	3661	TCCAGAGAGGAGCCTTAGCAGGAGTCCCTAGCCCTTTCACCCATACACATTTGGCTCAGG 3720
Qy	3721	GTTACCGAAGAGGGGCCAAGAAATTCAGAGTCCTCAGAAGAGAACTTATCTAGTGAGGATG 3780
Db	3721	GTTACCGAAGAGGGGCCAAGAAATTCAGAGTCCTCAGAAGAGAACTTATCTAGTGAGGATG 3780
Qy	3781	AAGAGCTTCCCTGCTTCCAAACACCTTGTTATTTGGTAAAGTAAACAATATACCTTCTCAGT 3840
Db	3781	AAGAGCTTCCCTGCTTCCAAACACCTTGTTATTTGGTAAAGTAAACAATATACCTTCTCAGT 3840
Qy	3841	CTACTAGGCATAGCACCGTTGCTTACCAGTGTCTGTCTAAGAACACAGAGGAGAAATTAT 3900
Db	3841	CTACTAGGCATAGCACCGTTGCTTACCAGTGTCTGTCTAAGAACACAGAGGAGAAATTAT 3900
Qy	3901	TATCATTTGAAGAAATAGCTTTAAATCAGCTGCAGTAACACAGGTAATAATTTGGCAAGGCAATCTC 3960
Db	3901	TATCATTTGAAGAAATAGCTTTAAATCAGCTGCAGTAACACAGGTAATAATTTGGCAAGGCAATCTC 3960
Qy	3961	AGGAACATCACCTTAGTGAGGAAACAAAATGTTCTGCTAGCTTGTGTTTTCTTCACAGTGCA 4020
Db	3961	AGGAACATCACCTTAGTGAGGAAACAAAATGTTCTGCTAGCTTGTGTTTTCTTCACAGTGCA 4020
Qy	4021	GTGAATTTGGAAGACTTGACTGCAAAATCAAAACCCAGGATCCCTTTCTTGATTTGGTTCCT 4080
Db	4021	GTGAATTTGGAAGACTTGACTGCAAAATCAAAACCCAGGATCCCTTTCTTGATTTGGTTCCT 4080
Qy	4081	CCAAACAAATCAGGCATCAGTCTCAAAAGCCAGGAGTTGGTCTGAGTGACAAGGAATTGG 4140
Db	4081	CCAAACAAATCAGGCATCAGTCTCAAAAGCCAGGAGTTGGTCTGAGTGACAAGGAATTGG 4140
Qy	4141	TTTCAGATGATGAAGAAAGAGAACGGGCTTTGGAAGAAAATAATCAAGAAAGCAAGCA 4200
Db	4141	TTTCAGATGATGAAGAAAGAGAACGGGCTTTGGAAGAAAATAATCAAGAAAGCAAGCA 4200
Qy	4201	TGGAATTCAAACTTAGGTGAAGCAGCATCTGGGTGTAGAGTGAAACAAAGCGTCTCTGAAG 4260
Db	4201	TGGAATTCAAACTTAGGTGAAGCAGCATCTGGGTGTAGAGTGAAACAAAGCGTCTCTGAAG 4260
Qy	4261	ACTGCTCAGGCTATCTCTCAGAGTGACATTTTAAACCATCTCAGCAGAGGATACCATGC 4320
Db	4261	ACTGCTCAGGCTATCTCTCAGAGTGACATTTTAAACCATCTCAGCAGAGGATACCATGC 4320
Qy	4321	AACATAACCTGATAAAGCTCCAGCAGGAAATGGCTGAACCTAGAGCTGTGTAGAACAGC 4380
Db	4321	AACATAACCTGATAAAGCTCCAGCAGGAAATGGCTGAACCTAGAGCTGTGTAGAACAGC 4380
Qy	4381	ATGGAGCCAGCCTTCTAACAGCTACCCCTCCATCATAGTGACTCTCTCTGCCCCTTGAGG 4440

4381	ATGGGACCGAGCCCTTTCAACAGCTACCCCTTCATCATAGTGA	CTCTCTGCGCCCTTGAGG	4444
Qy	4441	ACCTGCGAAATCCAGAACAAAGCACATCAGAAAAAGCAGTATTAACTTTACAGAAAAGTA	4500
	4441	ACCTGCGAAATCCAGAACAAAGCACATCAGAAAAAGCAGTATTAACTTTACAGAAAAGTA	4500
	4441	ACCTGCGAAATCCAGAACAAAGCACATCAGAAAAAGCAGTATTAACTTTACAGAAAAGTA	4500
Qy	4501	GTGAATACCCTTATAAGCCAGAAATCCAGAGGCCCTTTCTGCTGACAAGTTTGAGGTCTCTG	4560
	4501	GTGAATACCCTTATAAGCCAGAAATCCAGAGGCCCTTTCTGCTGACAAGTTTGAGGTCTCTG	4560
	4501	GTGAATACCCTTATAAGCCAGAAATCCAGAGGCCCTTTCTGCTGACAAGTTTGAGGTCTCTG	4560
Qy	4561	CAGATAGTCTTACCAGTAAAAATAAGAACCCAGAGTGGAAAGGTCA	4620
	4561	CAGATAGTCTTACCAGTAAAAATAAGAACCCAGAGTGGAAAGGTCA	4620
	4561	CAGATAGTCTTACCAGTAAAAATAAGAACCCAGAGTGGAAAGGTCA	4620
Qy	4621	GCCCATCAITTAGATGATAGTGGTACATGACACAGTTGCTCTGGAGTCTTTCAGAAATAGAA	4680
	4621	GCCCATCAITTAGATGATAGTGGTACATGACACAGTTGCTCTGGAGTCTTTCAGAAATAGAA	4680
	4621	GCCCATCAITTAGATGATAGTGGTACATGACACAGTTGCTCTGGAGTCTTTCAGAAATAGAA	4680
Qy	4681	ACTACCCATCTCAAGAGGAGCTCATTTAAGTTGTTGATGTGGAGGAGCAACAGCTGGAAG	4740
	4681	ACTACCCATCTCAAGAGGAGCTCATTTAAGTTGTTGATGTGGAGGAGCAACAGCTGGAAG	4740
	4681	ACTACCCATCTCAAGAGGAGCTCATTTAAGTTGTTGATGTGGAGGAGCAACAGCTGGAAG	4740
Qy	4741	AGTCTGGGCCACACAGATTTGCACGGAAACATCTTACTTTGCCAAGCGCAAGATCTAGAGGGAA	4800
	4741	AGTCTGGGCCACACAGATTTGCACGGAAACATCTTACTTTGCCAAGCGCAAGATCTAGAGGGAA	4800
	4741	AGTCTGGGCCACACAGATTTGCACGGAAACATCTTACTTTGCCAAGCGCAAGATCTAGAGGGAA	4800
Qy	4801	CCCCCTTACCTGGAATCTGGAAATCAGCCCTCTTCTCTGATGACCCCTGAACTCTGATCTCTG	4860
	4801	CCCCCTTACCTGGAATCTGGAAATCAGCCCTCTTCTCTGATGACCCCTGAACTCTGATCTCTG	4860
	4801	CCCCCTTACCTGGAATCTGGAAATCAGCCCTCTTCTCTGATGACCCCTGAACTCTGATCTCTG	4860
Qy	4861	AAGCAGAGCCCCAGAGTCAAGTCTGGTGTGGGAAACATACCATCTTCAACCTCTGCAATTGA	4920
	4861	AAGCAGAGCCCCAGAGTCAAGTCTGGTGTGGGAAACATACCATCTTCAACCTCTGCAATTGA	4920
	4861	AAGCAGAGCCCCAGAGTCAAGTCTGGTGTGGGAAACATACCATCTTCAACCTCTGCAATTGA	4920
Qy	4921	AAGTTCCCAATTCGAAGTTGCGAAGTCTGCCACAGGTCAGCTGCTGCTCATCACTACTG	4980
	4921	AAGTTCCCAATTCGAAGTTGCGAAGTCTGCCACAGGTCAGCTGCTGCTCATCACTACTG	4980
	4921	AAGTTCCCAATTCGAAGTTGCGAAGTCTGCCACAGGTCAGCTGCTGCTCATCACTACTG	4980
Qy	4981	ATACGTCTGGGTATAATGCAATGGAAGAAAGTGTGAGCAGGGAGAGACCCAGAAATTCACAG	5040
	4981	ATACGTCTGGGTATAATGCAATGGAAGAAAGTGTGAGCAGGGAGAGACCCAGAAATTCACAG	5040
	4981	ATACGTCTGGGTATAATGCAATGGAAGAAAGTGTGAGCAGGGAGAGACCCAGAAATTCACAG	5040
Qy	5041	CTTCAAACAGAAAGGGTCAAACAAAGAAATGTCATGTTGGTGTCTGGCTGACCCCGAGAAG	5100
	5041	CTTCAAACAGAAAGGGTCAAACAAAGAAATGTCATGTTGGTGTCTGGCTGACCCCGAGAAG	5100
	5041	CTTCAAACAGAAAGGGTCAAACAAAGAAATGTCATGTTGGTGTCTGGCTGACCCCGAGAAG	5100
Qy	5101	AAATTAATGCTCGTGTACAGTTTGCACAGAAACACCAACATCACTTTAACTTAATCTAATTA	5160
	5101	AAATTAATGCTCGTGTACAGTTTGCACAGAAACACCAACATCACTTTAACTTAATCTAATTA	5160
	5101	AAATTAATGCTCGTGTACAGTTTGCACAGAAACACCAACATCACTTTAACTTAATCTAATTA	5160
Qy	5161	CTGAAGAGACTACTCATGTTGTTATGAAAAACAGATGCTGAGTTTGTGTGAAACGGACAC	5220
	5161	CTGAAGAGACTACTCATGTTGTTATGAAAAACAGATGCTGAGTTTGTGTGAAACGGACAC	5220
	5161	CTGAAGAGACTACTCATGTTGTTATGAAAAACAGATGCTGAGTTTGTGTGAAACGGACAC	5220
Qy	5221	TGAAATATTTCTAGGAATTCGCGGAGGAAAAATGGGTAGTTAGCTATTTCTGGGTGACCC	5280
	5221	TGAAATATTTCTAGGAATTCGCGGAGGAAAAATGGGTAGTTAGCTATTTCTGGGTGACCC	5280
	5221	TGAAATATTTCTAGGAATTCGCGGAGGAAAAATGGGTAGTTAGCTATTTCTGGGTGACCC	5280
Qy	5281	AGTCTATTAAGAAAGAAAAATGCTGAATGAGCATGATTTTGAAGTCAGAGGAGATGTGG	5340
	5281	AGTCTATTAAGAAAGAAAAATGCTGAATGAGCATGATTTTGAAGTCAGAGGAGATGTGG	5340
	5281	AGTCTATTAAGAAAGAAAAATGCTGAATGAGCATGATTTTGAAGTCAGAGGAGATGTGG	5340
Qy	5341	TCAATGGAAGAAACCAACAAAGGTCCTAAGCGAGCAAGAGAAATCCAGGACAGAAAGATCT	5400
	5341	TCAATGGAAGAAACCAACAAAGGTCCTAAGCGAGCAAGAGAAATCCAGGACAGAAAGATCT	5400
	5341	TCAATGGAAGAAACCAACAAAGGTCCTAAGCGAGCAAGAGAAATCCAGGACAGAAAGATCT	5400
Qy	5401	TCAGGGGGCTAGAAATCTGTTGCTATGCGGCCCTTACCACATGCCACAGATCAACTGG	5460
	5401	TCAGGGGGCTAGAAATCTGTTGCTATGCGGCCCTTACCACATGCCACAGATCAACTGG	5460
	5401	TCAGGGGGCTAGAAATCTGTTGCTATGCGGCCCTTACCACATGCCACAGATCAACTGG	5460
Qy	5461	AATGGATGTTACAGCTGTGGTGCTCTCTGTGGTGAAGGAGCTTTTCATCTTCAACCCCTTG	5520
	5461	AATGGATGTTACAGCTGTGGTGCTCTCTGTGGTGAAGGAGCTTTTCATCTTCAACCCCTTG	5520
	5461	AATGGATGTTACAGCTGTGGTGCTCTCTGTGGTGAAGGAGCTTTTCATCTTCAACCCCTTG	5520

Qy 5521 GCACAGGTGTCCACCAATTGTTGCTGTCAGCCAGATGCTTGACAGAGGACAAATGGCT 5580  
 Db 5521 GCACAGGTGTCCACCAATTGTTGCTGTCAGCCAGATGCTTGACAGAGGACAAATGGCT 5580  
 Qy 5581 TCCATGCNAATGGGCGAGATGTGAGGACCTGTGGTGAACCCGAGAGTGGGTGTGACACA 5640  
 Db 5581 TCCATGCNAATGGGCGAGATGTGAGGACCTGTGGTGAACCCGAGAGTGGGTGTGACACA 5640  
 Qy 5641 GTGTAGCACTTACCACTGTCAGGAGCTGGACACCTACCTGATACCCAGATCCCCACA 5700  
 Db 5641 GTGTAGCACTTACCACTGTCAGGAGCTGGACACCTACCTGATACCCAGATCCCCACA 5700  
 Qy 5701 GCCACTACTGA 5711  
 Db 5701 GCCACTACTGA 5711

RESULT 3  
 ID AAV46448  
 XX AAV46448 standard; cDNA; 5711 BP.  
 AC AAV46448;  
 XX 18-NOV-1998 (first entry)  
 DT  
 XX Human BRCA1 omil cDNA.  
 XX  
 KW BRCA1; omil; human; breast and ovarian cancer predisposing gene;  
 KW polymorphism; susceptibility; anti-oncogene; tumour suppressor;  
 KW chromosome 17q; ss.  
 XX  
 OS Homo sapiens.  
 XX  
 FH Key Location/Qualifiers  
 FT CDS 120..5711  
 FT /\*tag= a  
 FT /product= "BRCA1 omil protein"  
 FT  
 XX  
 XX US5750400-A.  
 XX  
 PD 12-MAY-1998.  
 XX  
 XX 12-FEB-1997; 97US-0798691.  
 XX  
 PR 12-FEB-1996; 96US-0598591.  
 PR 12-FEB-1997; 97US-0798691.  
 XX  
 XX (ONCO-) ONCORMED INC.  
 XX  
 XX Allen AC, Alvares CP, Critz BS, Murphy PD, Olson SJ;  
 PI Schelter DB, Zeng B;  
 PI  
 XX WPI; 1998-296774/26.  
 DR  
 DR P-PSDB; AAW76098.  
 XX  
 XX BRCA1 omi gene coding sequences - useful for distinguishing between  
 PT polymorphisms and mutation(s) in the screening for disposition to  
 PT breast or ovarian cancer  
 XX  
 XX Claim 2d; Column 27-32; 54pp; English.  
 XX  
 XX This sequence encodes the human BRCA1 (breast and ovarian cancer  
 CC predisposing gene) omil gene. This sequence and polymorphic variations of  
 CC this sequence are useful for the identification of an individual who may  
 CC or may not have an increased susceptibility to breast or ovarian cancer.  
 CC The sequences used identify gene changes which are due to polymorphisms,  
 CC rather than cancer causing mutations. BRCA1 is an anti-oncogene (tumour  
 CC suppressor) which is involved in genetic inheritance of cancers,  
 CC especially breast and ovarian cancer. It is found at human chromosome 17q  
 CC which is known to be linked to cancer susceptibility, especially breast  
 CC cancer. Cells containing a mutation in this gene lose the wild-type  
 CC function of BRCA1 and are more susceptible to cancers.

XX  
 SQ Sequence 5711 BP; 1953 A; 1099 C; 1277 G; 1382 T; 0 other;  
 Query Match 100.0%; Score 5711; DB 19; Length 5711;  
 Best Local Similarity 100.0%; Pred. No. 0;  
 Matches 5711; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 Qy 1 AGCTCGCTGAGACTTCTCGACCCCGCACCAGGCTGGGGTTTCTCAGATAACTGGGCC 60  
 Db 1 AGCTCGCTGAGACTTCTCGACCCCGCACCAGGCTGGGGTTTCTCAGATAACTGGGCC 60  
 Qy 61 CTTGCGCTCAGGAGGCTTCCACCTCTGCTCTGGGTAAAGTTCAATTGGAACAGAAAGAAA 120  
 Db 61 CTTGCGCTCAGGAGGCTTCCACCTCTGCTCTGGGTAAAGTTCAATTGGAACAGAAAGAAA 120  
 Qy 121 TGGATTTATCTGCTCTTCGGGTTGAAGAAGTACAAAATGCTAATTAATCTATGAGAAAA 180  
 Db 121 TGGATTTATCTGCTCTTCGGGTTGAAGAAGTACAAAATGCTAATTAATCTATGAGAAAA 180  
 Qy 181 TCTTAGAGTGTCCCATCTGCTGAGTTGATCAAGGAACCTGTCTCCACAAGTGTGACC 240  
 Db 181 TCTTAGAGTGTCCCATCTGCTGAGTTGATCAAGGAACCTGTCTCCACAAGTGTGACC 240  
 Qy 241 ACATATTTTGCATAATTTTGCATGCTGAACTTCTCAACAGAGAAAGGCTTTCACAGT 300  
 Db 241 ACATATTTTGCATAATTTTGCATGCTGAACTTCTCAACAGAGAAAGGCTTTCACAGT 300  
 Qy 301 GTCTTTTATGATAGATGATATAACAAAGAGGCTTACAAAGAAAGTACAGATTTAGTC 360  
 Db 301 GTCTTTTATGATAGATGATATAACAAAGAGGCTTACAAAGAAAGTACAGATTTAGTC 360  
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 Db 361 AACTTTTGAAGAGCTATTGAAATCATTTTGTGCTTTTTCAGTTTGACACAGTTTGGAGT 420  
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 Db 421 ATGCAAAACAGCTATTAATTTTGCATAAAGGAAATACTCTCTGTAACATCTTAAAGATG 480  
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 Db 481 AAGTTTCTATCATCCAAAGTATGGGCTACAGAAACCGTGCCAAAGACTTCTACAGAGTG 540  
 Qy 541 AACCCGAAATCTTCTCTGAGGAAACAGTCTCAGTGTCCAACTCTTAACCTTGGAA 600  
 Db 541 AACCCGAAATCTTCTCTGAGGAAACAGTCTCAGTGTCCAACTCTTAACCTTGGAA 600  
 Qy 601 CTGTGAGAACTCTGAGGACAAAGCAGCGGATACAACTCAAAAGACCTCTGTCTACATTG 660  
 Db 601 CTGTGAGAACTCTGAGGACAAAGCAGCGGATACAACTCAAAAGACCTCTGTCTACATTG 660  
 Qy 661 AATTGGGATCTGATTTCTTCTGAAGATACCGTTAATAGGCAACTTATTGAGTGTGGAG 720  
 Db 661 AATTGGGATCTGATTTCTTCTGAAGATACCGTTAATAGGCAACTTATTGAGTGTGGAG 720  
 Qy 721 ATCAAGAAATTTTACAAATCACCCCTCAAGGAACCGGATGAATCAGTTTGGATTCTG 780  
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 Qy 781 CAAAAAAGGCTGCTTGTGAATTTTCTGAGACGGATGTAAACAAATFACTGAACATCATCAAC 840  
 Db 781 CAAAAAAGGCTGCTTGTGAATTTTCTGAGACGGATGTAAACAAATFACTGAACATCATCAAC 840  
 Qy 841 CCAGTAAATATGATTTGAAACACCACTGAGAGGCTGAGAGGCTCCAGAAAGT 900  
 Db 841 CCAGTAAATATGATTTGAAACACCACTGAGAGGCTGAGAGGCTCCAGAAAGT 900  
 Qy 901 ATCAGGCTAGTCTGTGTTTCAAACTGCTGAGGCTGAGGCTGAGGCTGAGGCTGAGGCT 960  
 Db 901 ATCAGGCTAGTCTGTGTTTCAAACTGCTGAGGCTGAGGCTGAGGCTGAGGCTGAGGCT 960  
 Qy 961 GCTCATTACAGCTAGAGAAACAGCAGTTTATTCTCACTAAAGACAGAAATGAGAA 1020  
 Db 961 GCTCATTACAGCTAGAGAAACAGCAGTTTATTCTCACTAAAGACAGAAATGAGAA 1020

Db 961 GCTCATTTACAGCATGAGAACAGCAGTGTATTATCTCACTAAAGACAGAAATGTTAGAAA 1020  
Qy 1021 AGGCTGAATTTCTGTAATATAAAGCAAACAGCCTGGCTTTAGCAAGGAGCCAAACATAACAGAT 1080  
Db 1021 AGGCTGAATTTCTGTAATATAAAGCAAACAGCCTGGCTTTAGCAAGGAGCCAAACATAACAGAT 1080  
Qy 1081 GGCTGGAAGTAAAGAAACATGTAATGATAGGGGGACTCCAGCACAGAAAGAGGTAG 1140  
Db 1081 GGCTGGAAGTAAAGAAACATGTAATGATAGGGGGACTCCAGCACAGAAAGAGGTAG 1140  
Qy 1141 ATCTGAATGCTGATCCCTCTGTGTGAGAGAAAGAAATGGAATAAGCAGAGAACTGCCATGCT 1200  
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Qy 1201 CAGAGAACTCTAGAGATPACTGAAGATGTTCTCTGGATAACACATAAATPAGCAGCATTCAGA 1260  
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Qy 1261 AGTTAATGATGGTGTTCAGAAAGTGAATGAACTGTTAGTTAGGTTCTGATGACTCAATGATG 1320  
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Qy 1441 TATGTAAAGTGAAGAGTTTCACTCCAAATCAGTAGAGAGTAATATTTGAAGACAAAATAT 1500  
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Db 1561 TAATTTAGGAGCATTTGTTACTGAGCCACAGATAATACAGAGCGTCCCTCCACAATA 1620  
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Db 1861 AAACGAAAGCTGAACCTTAAAGAGCAGTATAAGCAATATGGAATCTGAAATTAATATCC 1920  
Qy 1921 ACAATTCAAAGACACCTTAAAGAAATAGGCTGAGGAGGAGTCTTTTACACAGGCAATTC 1980  
Db 1921 ACAATTCAAAGACACCTTAAAGAAATAGGCTGAGGAGGAGTCTTTTACACAGGCAATTC 1980  
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Qy 2521 GTGTGAGTCACTGTCAGCAGCATTTGAAACCCCAAGGACCTAAATTCATGTTGTTCCAAAG 2580  
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QY 3181 GTACAGTGAGCACAAATAGCCGTAAATAACATTAGAGAAAATGTTTTAAAGGAGCCAGCT 3240  
DB 3181 GTACAGTGAGCACAAATAGCCGTAAATAACATTAGAGAAAATGTTTTAAAGGAGCCAGCT 3240  
QY 3241 CAAGCAATATTAATGAAGTAGGTTCCAGTACTAATGAAGTGGGCTCCAGTATTAATGAAA 3300  
DB 3241 CAAGCAATATTAATGAAGTAGGTTCCAGTACTAATGAAGTGGGCTCCAGTATTAATGAAA 3300  
QY 3301 TAGGTTCCAGTGATGAAGAACATTCAGCAGAACCTAGGTAGAGAACAGAGGGGCCAAATTTGA 3360  
DB 3301 TAGGTTCCAGTGATGAAGAACATTCAGCAGAACCTAGGTAGAGAACAGAGGGGCCAAATTTGA 3360  
QY 3361 ATGCTATGCTTAGATTTAGGGGTTTTGCAACCTGAGGCTCTATAAACAAGTCTTCCCTGGAA 3420  
DB 3361 ATGCTATGCTTAGATTTAGGGGTTTTGCAACCTGAGGCTCTATAAACAAGTCTTCCCTGGAA 3420  
QY 3421 GTAATTTGATGATCTCTGAATAAATAAAGCAAGAAATATGAAGAAATAGTTCAGACTGTTA 3480  
DB 3421 GTAATTTGATGATCTCTGAATAAATAAAGCAAGAAATATGAAGAAATAGTTCAGACTGTTA 3480  
QY 3481 ATACAGATTTCTCTCCATATCTGATTTTCAGATACCTTAGACAGCCTATGGGAGTAGTC 3540  
DB 3481 ATACAGATTTCTCTCCATATCTGATTTTCAGATACCTTAGACAGCCTATGGGAGTAGTC 3540  
QY 3541 ATGCATCTCAGGTTTGTCTGAGACACCTGATGACCTGTTAGATGATGGTGAATAAAGG 3600  
DB 3541 ATGCATCTCAGGTTTGTCTGAGACACCTGATGACCTGTTAGATGATGGTGAATAAAGG 3600  
QY 3601 AAGTACTAGTTTGTGTAATAAGCAATTAAGAAAGTTCTGCTGTTTTAGCAAAAGCG 3660  
DB 3601 AAGTACTAGTTTGTGTAATAAGCAATTAAGAAAGTTCTGCTGTTTTAGCAAAAGCG 3660  
QY 3661 TCCAGAGAGGAGCTTAGCAGGAGTCTAGCCCTTTTCCATACACATTTGGCTCAGG 3720  
DB 3661 TCCAGAGAGGAGCTTAGCAGGAGTCTAGCCCTTTTCCATACACATTTGGCTCAGG 3720  
QY 3721 GTTACCGAAGAGGGGCCAAAGAAATAGAGTCCCTCAGAAAGAGAACTTATCTAGTGAGGATG 3780  
DB 3721 GTTACCGAAGAGGGGCCAAAGAAATAGAGTCCCTCAGAAAGAGAACTTATCTAGTGAGGATG 3780  
QY 3781 AAGAGCTTCCGTGTTCCAACTGTTTATTTGGTAAAGTAAACAATATACCTTCTCAGT 3840  
DB 3781 AAGAGCTTCCGTGTTCCAACTGTTTATTTGGTAAAGTAAACAATATATACCTTCTCAGT 3840  
QY 3841 CTACTAGGCATAGCACCGTTGCTACCGAGTGTCTGCTTAAGAACACAGAGGAGAAATTTAT 3900  
DB 3841 CTACTAGGCATAGCACCGTTGCTACCGAGTGTCTGCTTAAGAACACAGAGGAGAAATTTAT 3900  
QY 3901 TATCATTGAAGAATAGCTTAAATGACTGCAGTAAACCAAGGTAAATTTGGCAAGGCATCTC 3960  
DB 3901 TATCATTGAAGAATAGCTTAAATGACTGCAGTAAACCAAGGTAAATTTGGCAAGGCATCTC 3960  
QY 3961 AGGAACATACCTTAGTGAGAGAAACAAATTTCTGCTAGCTTGTGTTTTCTTCAAGTGCA 4020  
DB 3961 AGGAACATACCTTAGTGAGAGAAACAAATTTCTGCTAGCTTGTGTTTTCTTCAAGTGCA 4020  
QY 4021 GTGAATTTGAAGACTTCTGACTGCAAAATACAAACCCAGGATCCTTCTGATTTGGTTCTT 4080  
DB 4021 GTGAATTTGAAGACTTCTGACTGCAAAATACAAACCCAGGATCCTTCTGATTTGGTTCTT 4080  
QY 4081 CCAAAACAAATGAGGCATCAGTCTGAAAGCCAGGAGTTGGTCTGAGTGACAAGGAATTGG 4140  
DB 4081 CCAAAACAAATGAGGCATCAGTCTGAAAGCCAGGAGTTGGTCTGAGTGACAAGGAATTGG 4140  
QY 4141 TTTCAGATGATGAAGAAAGGAAACCGGCTTGGAAAGAAATATCAAGAAAGACAAAGCA 4200  
DB 4141 TTTCAGATGATGAAGAAAGGAAACCGGCTTGGAAAGAAATATCAAGAAAGACAAAGCA 4200  
QY 4201 TGGATTCAAACTTAGGTGAAGCAGCATCTCGGTTGTGAGAGTGAAACAAGCGTCTCTGAAG 4260  
DB 4201 TGGATTCAAACTTAGGTGAAGCAGCATCTCGGTTGTGAGAGTGAAACAAGCGTCTCTGAAG 4260  
QY 4261 ACTGCTCAGGGCTATCCTCTCAGAGTGACATTTTAAACCACTCAGCAGAGGGGATACCATGC 4320

DB 4261 ACTGCTCAGGGCTATCCTCTCAGAGTGACATTTTAAACCACTCAGCAGAGGGATACCATGC 4320  
QY 4321 AACATAACCTGATAAAGCTCCAGCAGGAAATGCGTGAAGCTAGAGCTGTGTTGAAACAGC 4380  
DB 4321 AACATAACCTGATAAAGCTCCAGCAGGAAATGCGTGAAGCTAGAGCTGTGTTGAAACAGC 4380  
QY 4381 ATGGGAGCCAGCCTTCTAACAGCTACCTTCCATCATTAAGTACTCTCTGCCCTTGAGG 4440  
DB 4381 ATGGGAGCCAGCCTTCTAACAGCTACCTTCCATCATTAAGTACTCTCTGCCCTTGAGG 4440  
QY 4441 ACCTGCGAAATCCAGAAACAAAGCACATCAGAAAAAGCAGTATTAACTTTCACAGAAAAAGTA 4500  
DB 4441 ACCTGCGAAATCCAGAAACAAAGCACATCAGAAAAAGCAGTATTAACTTTCACAGAAAAAGTA 4500  
QY 4501 GTGAATACCTTATAAGCCAGAAATCCAGAAAGCCTTTCTGCTGACAAGTTTGAAGTGTCTG 4560  
DB 4501 GTGAATACCTTATAAGCCAGAAATCCAGAAAGCCTTTCTGCTGACAAGTTTGAAGTGTCTG 4560  
QY 4561 CAGATAGTTCTACACGCTTAAATAAAGAACAGAGGTGGAAGGTCAATCCCTTCTTAAT 4620  
DB 4561 CAGATAGTTCTACACGCTTAAATAAAGAACAGAGGTGGAAGGTCAATCCCTTCTTAAT 4620  
QY 4621 GCCCATCATTTAGATGATAGTGTGTACATGCACAGTTGCTCTGGAGTCTTTCAGAAATAGAA 4680  
DB 4621 GCCCATCATTTAGATGATAGTGTGTACATGCACAGTTGCTCTGGAGTCTTTCAGAAATAGAA 4680  
QY 4681 ACTACCCATCTCAAGAGGAGCTCATTAAGGTTGTGATGTGGAGGAGCAACAGCTGGAAG 4740  
DB 4681 ACTACCCATCTCAAGAGGAGCTCATTAAGGTTGTGATGTGGAGGAGCAACAGCTGGAAG 4740  
QY 4741 AGTCTGGGCCACACAGATTTTACCGGAACATCTTACTTTCGCCAAGCAGATCTAGAGGGAA 4800  
DB 4741 AGTCTGGGCCACACAGATTTTACCGGAACATCTTACTTTCGCCAAGCAGATCTAGAGGGAA 4800  
QY 4801 CCCCTTACCTTGGAAATCTGGAATCAGCCTCTTCTCTGATGACCCCTGAAATCTGATCTTCTG 4860  
DB 4801 CCCCTTACCTTGGAAATCTGGAATCAGCCTCTTCTCTGATGACCCCTGAAATCTGATCTTCTG 4860  
QY 4861 AAGACAGAGCCCCAGAGTCTGAGTCTGTTGGCAACATACCATCTTCAACCTCTGCATCTGA 4920  
DB 4861 AAGACAGAGCCCCAGAGTCTGAGTCTGTTGGCAACATACCATCTTCAACCTCTGCATCTGA 4920  
QY 4921 AAGTCTCCCAATTTGAAAGTTGACAGATCTGCCAGAGGTCCAGCTGCTCATCTACTACTG 4980  
DB 4921 AAGTCTCCCAATTTGAAAGTTGACAGATCTGCCAGAGGTCCAGCTGCTCATCTACTACTG 4980  
QY 4981 ATACTGCTGGGTATAATGCAATGGAAGAAAGTGTGAGCAGGAGAGAGCCAGAAATTTGACAG 5040  
DB 4981 ATACTGCTGGGTATAATGCAATGGAAGAAAGTGTGAGCAGGAGAGAGCCAGAAATTTGACAG 5040  
QY 5041 CTTTCAACAGAAAGGGTCAACAAAGAAATGTCCATGTTGGTGTCTGGCTTGACCCCAAGAG 5100  
DB 5041 CTTTCAACAGAAAGGGTCAACAAAGAAATGTCCATGTTGGTGTCTGGCTTGACCCCAAGAG 5100  
QY 5101 AATTTATGCTCGTGTAACAGTTTGGCAGAAAAACACCACTCACTTTAACTAACTTAATTA 5160  
DB 5101 AATTTATGCTCGTGTAACAGTTTGGCAGAAAAACACCACTCACTTTAACTAACTTAATTA 5160  
QY 5161 CTGAAGAGACTACTCATGTTGTTTATGAAAAACAGATGCTGAGTTTGTGTGTAACCGGACAC 5220  
DB 5161 CTGAAGAGACTACTCATGTTGTTTATGAAAAACAGATGCTGAGTTTGTGTGTAACCGGACAC 5220  
QY 5221 TGAATATTTTTCTAGGAAATTCGGGAGGAAAAATGGGTAGTTAGTATTTCTGGGTGACCC 5280  
DB 5221 TGAATATTTTTCTAGGAAATTCGGGAGGAAAAATGGGTAGTTAGTATTTCTGGGTGACCC 5280  
QY 5281 AGTCTATTTAAAGAAAGAAATGCTCAATCAGCATGATTTTGAAGTCAGAGGAGATGTGG 5340  
DB 5281 AGTCTATTTAAAGAAAGAAATGCTCAATCAGCATGATTTTGAAGTCAGAGGAGATGTGG 5340  
QY 5341 TCAATGGAAGAAACCAACCAAGGTCTCAAGCGAGCAAGAGAAATCCCAAGGACAGAAAGATCT 5400

Db 5341 TCAATGGAAGAACCAAGGTCCTCAAGGAGCAAGAGAAATCCAGGACAGAAAGATCT 5400  
 Qy 5401 TCAGGGGGCTAGAAATCTGTGCTATGGGCCCTTCAACCAATGCCACAGATCAACTGG 5460  
 Db 5401 TCAGGGGGCTAGAAATCTGTGCTATGGGCCCTTCAACCAATGCCACAGATCAACTGG 5460  
 Qy 5461 AATGATGGTACAGCTGTGGTCTTCTGTGGTGAAGGAGCTTTCATCATCACCCTTG 5520  
 Db 5461 AATGATGGTACAGCTGTGGTCTTCTGTGGTGAAGGAGCTTTCATCATCACCCTTG 5520  
 Qy 5521 GCACAGGTGTCCACCAATGTGTGTGTGCAGCCAGATGCTGCAGACAGAGACAAATGGCT 5580  
 Db 5521 GCACAGGTGTCCACCAATGTGTGTGTGCAGCCAGATGCTGCAGACAGAGACAAATGGCT 5580  
 Qy 5581 TCCATGCAATGGGCAGATGTGTGAGGCACCTGTGGTGACCCGAGAGTGGGTGTGGACA 5640  
 Db 5581 TCCATGCAATGGGCAGATGTGTGAGGCACCTGTGGTGACCCGAGAGTGGGTGTGGACA 5640  
 Qy 5641 GTGTAGCACTTACAGTGCAGGAGCTGGACACCTTACCTGATACCCGAGATCCCCACA 5700  
 Db 5641 GTGTAGCACTTACAGTGCAGGAGCTGGACACCTTACCTGATACCCGAGATCCCCACA 5700  
 Qy 5701 GCCACTACTGA 5711  
 Db 5701 GCCACTACTGA 5711

## RESULT 4

AAC60793  
 ID AAC60793 standard; cDNA; 5711 BP.  
 XX  
 AC AAC60793;  
 DT 07-FEB-2001 (first entry)  
 XX  
 DE Human BRCA1 (om1) nucleotide sequence SEQ ID NO:1.  
 XX  
 KW Human; BRCA1; chromosome 17; 17q21; breast cancer; ovarian cancer;  
 KW gene therapy; diagnosis; cytostatic; genetic susceptibility; mutation;  
 KW polymorphism; identification; ss.  
 XX Homo sapiens.  
 XX  
 XX US6130322-A.  
 XX  
 XX 10-OCT-2000.  
 XX  
 XX 06-MAY-1998; 98US-0074476.  
 XX  
 XX 12-FEB-1996; 96US-0598591.  
 XX  
 XX 12-DEC-1997; 97US-0798691.  
 XX  
 XX (GENE-) GENE LOGIC INC.  
 XX  
 XX Zeng B, Thurber D, Olson SJ, Alvares CP, Allen ACP, Murphy PD;  
 PI Critz BS;  
 XX  
 XX WPI; 2000-646756/62.  
 XX  
 XX P-PSDB; AAB24217.  
 XX  
 XX New coding sequence of the human BRCA1 gene, i.e. BRCA1 (om12), useful  
 XX in gene therapy, especially for preventing or treating breast or  
 XX ovarian cancer, as well as for diagnosing or monitoring breast or  
 XX ovarian cancer -  
 XX  
 XX Example 2; Column 29-36; 56pp; English.  
 XX  
 XX AAC60793 to AAC60795 encode the human BRCA1 (om1-3) proteins given in  
 XX AAB24217 to AAB24219 respectively. BRCA1 is found on chromosome 17  
 XX mapping to position 17q21. The BRCA1 (om12) coding sequence is  
 XX specifically claimed in the present invention. The BRCA1 (om12) coding  
 XX sequence is useful in gene therapy, especially for preventing or treating  
 XX breast or ovarian cancer. It is also useful for diagnosing or monitoring

CC breast or ovarian cancer. Furthermore, the BRCA1 (om12) coding sequence  
 CC is useful for: (a) identifying individuals having BRCA1 gene mutations  
 CC and having an increased genetic susceptibility to breast or ovarian  
 CC cancer, or identifying a mutation that increases the genetic  
 CC susceptibility to breast or ovarian cancer; (b) avoiding  
 CC misinterpretation of polymorphisms found in the BRCA1 gene; (c)  
 CC determining the presence of a previously unknown mutation in the BRCA1  
 CC gene; (d) probing a human sample of the BRCA1 gene by allele to determine  
 CC the presence of either polymorphic alleles or mutations; and (e)  
 CC performing diagnosis with a reagent derived from the BRCA1 (om1) cDNA  
 CC sequence. AAC60796 to AAC60861 represent PCR primers for the BRCA1 gene,  
 CC which are used in an example from the present invention.  
 XX  
 SQ Sequence 5711 BP; 1953 A; 1099 C; 1277 G; 1382 T; 0 other;  
 Query Match 100.0%; Score 5711; DB 21; Length 5711;  
 Best Local Similarity 100.0%; Pred. No. 0;  
 Matches 5711; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 Qy 1 AGTTCGTGAGACTTCTGGACCCCGCACAGGCTGTGGGTTTCTCAGATAACTGGGCC 60  
 Db 1 AGTTCGTGAGACTTCTGGACCCCGCACAGGCTGTGGGTTTCTCAGATAACTGGGCC 60  
 Qy 61 CCTGCGCTCAGGAGGCTTCAACCTCTGCTTGGTAAAGTTTCAATGGACAGAAAGAA 120  
 Db 61 CCTGCGCTCAGGAGGCTTCAACCTCTGCTTGGTAAAGTTTCAATGGACAGAAAGAA 120  
 Qy 121 TGGATTTATCTGCTCTTGGGTTGAAGAAGTACAAAATGTCAATTAATGCTATGAGAAA 180  
 Db 121 TGGATTTATCTGCTCTTGGGTTGAAGAAGTACAAAATGTCAATTAATGCTATGAGAAA 180  
 Qy 181 TCTTAGAGTGTCCCATCTGTCTGGAGTTGATCAAGGAACCTGTCTCCACAAAGTGTGACC 240  
 Db 181 TCTTAGAGTGTCCCATCTGTCTGGAGTTGATCAAGGAACCTGTCTCCACAAAGTGTGACC 240  
 Qy 241 ACATATTTTGCATTTTGGATGTGAACTTCTCAACACAGAAAGGGGCTTTCACAGT 300  
 Db 241 ACATATTTTGCATTTTGGATGTGAACTTCTCAACACAGAAAGGGGCTTTCACAGT 300  
 Qy 301 GTCTTTTGTAGTAAGTATATAACCAAAAGGAGCTTACAGAAAGTACAGATTTAGTTC 360  
 Db 301 GTCTTTTGTAGTAAGTATATAACCAAAAGGAGCTTACAGAAAGTACAGATTTAGTTC 360  
 Qy 361 AACTTTTGAAGAGCTATTGAAATCAATTTGTGCTTTTTCAGCTTTCAGACAGTGTGGAGT 420  
 Db 361 AACTTTTGAAGAGCTATTGAAATCAATTTGTGCTTTTTCAGCTTTCAGACAGTGTGGAGT 420  
 Qy 421 ATGCAAAACAGCTATAATTTTGCACAAAAGGAAATTAATCTCTCTGAAACATCTAAAGATG 480  
 Db 421 ATGCAAAACAGCTATAATTTTGCACAAAAGGAAATTAATCTCTCTGAAACATCTAAAGATG 480  
 Qy 481 AAGTTTCTATCATCCAAAGTATGGCTACAGAAACCGTCCCAAAAGACTTCTACAGAGTG 540  
 Db 481 AAGTTTCTATCATCCAAAGTATGGCTACAGAAACCGTCCCAAAAGACTTCTACAGAGTG 540  
 Qy 541 AACCCGAAAATCCCTTCTTGCAGGAAACAGCTCTCAGTGTCCAACTCTCTAACCTTGGAA 600  
 Db 541 AACCCGAAAATCCCTTCTTGCAGGAAACAGCTCTCAGTGTCCAACTCTCTAACCTTGGAA 600  
 Qy 601 CTGTGAGAACTCTGAGGACAAAAGCAGGGATACAACTCTCAAAAGACGCTGTCTACATTTG 660  
 Db 601 CTGTGAGAACTCTGAGGACAAAAGCAGGGATACAACTCTCAAAAGACGCTGTCTACATTTG 660  
 Qy 661 AATTGGGATCTGATTTCTTGAAGATACCGTTAATAGGCAACTTATTGCAAGTGTGGAG 720  
 Db 661 AATTGGGATCTGATTTCTTGAAGATACCGTTAATAGGCAACTTATTGCAAGTGTGGAG 720  
 Qy 721 ATCAAGAAATGTTTACAAATCAACCTCAAGGAAACAGGGATCAAAATCAGTTTGAATCTG 780  
 Db 721 ATCAAGAAATGTTTACAAATCAACCTCAAGGAAACAGGGATCAAAATCAGTTTGAATCTG 780  
 Qy 781 CAAAAAAGGCTGTGTGAAATTTTCTGAGACGGATGTAAACAAATCTGAAACATCATCAAC 840  
 Db 781 CAAAAAAGGCTGTGTGAAATTTTCTGAGACGGATGTAAACAAATCTGAAACATCATCAAC 840

Db 781 CAAAAAGGCTGCTGTGTAATTTCTGAGACGATGTAAACAAATCTCAACATCATCAAC 840  
Qy CCAGTAAATATGATTTGAAACCACTGAGAGCGTGCAGCTGAGAGCATCCAGAAAGT 900  
Db 841 CCAAGTAAATATGATTTGAAACCACTGAGAGCGTGCAGCTGAGAGCATCCAGAAAGT 900  
Qy 901 ATCAGGCTAGTTCCTGTTTCAAACCTTGCATGTGGAGCCATGTGGCACAATACTCATGCCA 960  
Db 901 ATCAGGCTAGTTCCTGTTTCAAACCTTGCATGTGGAGCCATGTGGCACAATACTCATGCCA 960  
Qy 961 GCTCATTTACAGCATGAGAACAGCAGTTTTACTCTAATAAGACAGAAATGATAGAAA 1020  
Db 961 GCTCATTTACAGCATGAGAACAGCAGTTTTACTCTAATAAGACAGAAATGATAGAAA 1020  
Qy 1021 AGGCTGAATTCCTGTAATAAAGCAACAGCCTGCTTAGCAAGGAGCCACATACACAGAT 1080  
Db 1021 AGGCTGAATTCCTGTAATAAAGCAACAGCCTGCTTAGCAAGGAGCCACATACACAGAT 1080  
Qy 1081 GGGCTGGAAGTAAAGAAACATGTAAATGATGGCGGACTCCAGCAGACAGAAAAAGGTAG 1140  
Db 1081 GGGCTGGAAGTAAAGAAACATGTAAATGATGGCGGACTCCAGCAGACAGAAAAAGGTAG 1140  
Qy 1141 ATCTGAATGCTGATCCCTGTGTGAGAGAAAGAAATGGAATAGCAGAACTGCGATGCT 1200  
Db 1141 ATCTGAATGCTGATCCCTGTGTGAGAGAAAGAAATGGAATAGCAGAACTGCGATGCT 1200  
Qy 1201 CAGAGAACTCTAGAGATACTGAAGATGTTCTGTTAGGTTCTGATGACTCAATGATG 1260  
Db 1201 CAGAGAACTCTAGAGATACTGAAGATGTTCTGTTAGGTTCTGATGACTCAATGATG 1260  
Qy 1261 AAGTTAATGATGCTGTTTCCAGAAAGTGAATGTTAGGTTCTGATGACTCAATGATG 1320  
Db 1261 AAGTTAATGATGCTGTTTCCAGAAAGTGAATGTTAGGTTCTGATGACTCAATGATG 1320  
Qy 1321 GGGAGTCTGAATCAAATGCCAAAGTAGCTGATGTTATTTGGACGTTCTAAATGAGGTAGT 1380  
Db 1321 GGGAGTCTGAATCAAATGCCAAAGTAGCTGATGTTATTTGGACGTTCTAAATGAGGTAGT 1380  
Qy 1381 AATATTCTGTTCTTTCAGAGAAATAGACTTACTGGCCAGTGATCTCATGAGGCTTTAA 1440  
Db 1381 AATATTCTGTTCTTTCAGAGAAATAGACTTACTGGCCAGTGATCTCATGAGGCTTTAA 1440  
Qy 1441 TATGTAAAGTGAAGAGTTCACCTCCAAATCAGTAGAGAGTAATATTTGAAGACAAATAT 1500  
Db 1441 TATGTAAAGTGAAGAGTTCACCTCCAAATCAGTAGAGAGTAATATTTGAAGACAAATAT 1500  
Qy 1501 TTGGGAAAACCTATCGGAAGAGGCAAGCCTCCCAATCTTAAGCCATGTAACTGAAAATC 1560  
Db 1501 TTGGGAAAACCTATCGGAAGAGGCAAGCCTCCCAATCTTAAGCCATGTAACTGAAAATC 1560  
Qy 1561 TAAATTATAGGACATTTGTTTACTGAGCCACAGATAATACAGAGCGTCCCTCACAATA 1620  
Db 1561 TAAATTATAGGACATTTGTTTACTGAGCCACAGATAATACAGAGCGTCCCTCACAATA 1620  
Qy 1621 AATTAAAGCGTAAAGGAGACCTACATCAGCGCTTCACTCTGAGGATTTTATCAAGAAAG 1680  
Db 1621 AATTAAAGCGTAAAGGAGACCTACATCAGCGCTTCACTCTGAGGATTTTATCAAGAAAG 1680  
Qy 1681 CAGATTTGGCAGTTCAAAGAATCTCTGAATGATTAATACAGGAACTAAACAAACGGAGC 1740  
Db 1681 CAGATTTGGCAGTTCAAAGAATCTCTGAATGATTAATACAGGAACTAAACAAACGGAGC 1740  
Qy 1741 AGAATGCTCAAGTGAATTAATTAATAGTGTCTATGAGATTAACCAAAAGGTGATTT 1800  
Db 1741 AGAATGCTCAAGTGAATTAATTAATAGTGTCTATGAGATTAACCAAAAGGTGATTT 1800  
Qy 1801 CTATTCAAGATGAGAAAAATCTTAACCAATAGAAATCACTCGAAAAAGAAATCTGCTTTCA 1860  
Db 1801 CTATTCAAGATGAGAAAAATCTTAACCAATAGAAATCACTCGAAAAAGAAATCTGCTTTCA 1860  
Qy 1861 AAACGAAAGCTGAACCTTATAGCGAGAGTATAGCAATATGGAATCTGAATTAATATCC 1920  
Db 1861 AAACGAAAGCTGAACCTTATAGCGAGAGTATAGCAATATGGAATCTGAATTAATATCC 1920

Qy 1921 ACAATTCAAAAGCACCTAAAAAGAAATAGGCTGAGAGGAAGTCTTTTACCAAGGCATATTC 1980  
Db 1921 ACAATTCAAAAGCACCTAAAAAGAAATAGGCTGAGAGGAAGTCTTTTACCAAGGCATATTC 1980  
Qy 1981 ATGCGCTTGAACCTAGTAGTACAGTAGAAATCTAAGCCCACTAAATTTGTAATGCAAA 2040  
Db 1981 ATGCGCTTGAACCTAGTAGTACAGTAGAAATCTAAGCCCACTAAATTTGTAATGCAAA 2040  
Qy 2041 TTGATAGTGTCTTAGCAGTGAAGAGATAAGAAAAAAGTACAAACAAATGCGAGTCA 2100  
Db 2041 TTGATAGTGTCTTAGCAGTGAAGAGATAAGAAAAAAGTACAAACAAATGCGAGTCA 2100  
Qy 2101 GGCACACAGAAACCTTCACTCACTGAAAGTAAAGAACCTGCAACTGGAGCCCAAGAGA 2160  
Db 2101 GGCACACAGAAACCTTCACTCACTGAAAGTAAAGAACCTGCAACTGGAGCCCAAGAGA 2160  
Qy 2161 GTAAACAGCCAAATGAACAGACAAAGTAAAGACATGACAGTGATATTTTCCAGAGCTGA 2220  
Db 2161 GTAAACAGCCAAATGAACAGACAAAGTAAAGACATGACAGTGATATTTTCCAGAGCTGA 2220  
Qy 2221 AGTTAAACAAATGCACTGCTGTTCTTTTACTAAGTGTTCATAATACCAAGTGAACCTTAAAGAA 2280  
Db 2221 AGTTAAACAAATGCACTGCTGTTCTTTTACTAAGTGTTCATAATACCAAGTGAACCTTAAAGAA 2280  
Qy 2281 TTGTCATCTAGCCTTCCAAAGAGAGAAAAAGAGAGAACTAGAAACAGTATTAAGTGT 2340  
Db 2281 TTGTCATCTAGCCTTCCAAAGAGAGAAAAAGAGAGAACTAGAAACAGTATTAAGTGT 2340  
Qy 2341 CTAAATATGCTGAAGACCCCAAGATCTCAATGTTAAGTGGAGAAAGGTTTTCACAACTG 2400  
Db 2341 CTAAATATGCTGAAGACCCCAAGATCTCAATGTTAAGTGGAGAAAGGTTTTCACAACTG 2400  
Qy 2401 AAAGATCTGTAGAGAGTAGCAGTATTTTCACTGGTACCTGGTACTGATTTATGGCACTCAGG 2460  
Db 2401 AAAGATCTGTAGAGAGTAGCAGTATTTTCACTGGTACCTGGTACTGATTTATGGCACTCAGG 2460  
Qy 2461 AAAGTATCTGTTTACTGGAAAGTTAGCACTCTAGGAGGCAAAAAACAGAACCAATAAAT 2520  
Db 2461 AAAGTATCTGTTTACTGGAAAGTTAGCACTCTAGGAGGCAAAAAACAGAACCAATAAAT 2520  
Qy 2521 GTGTGAGTCAAGTGTGACGATTTGAAAAACCCCAAGGACCTAAATTCATGTTGTTTCCAAAG 2580  
Db 2521 GTGTGAGTCAAGTGTGACGATTTGAAAAACCCCAAGGACCTAAATTCATGTTGTTTCCAAAG 2580  
Qy 2581 ATAAATAGAAATGACACAGAAAGGCTTTAAGTATCCATTGGGACATGAAGTTAAACACAGTC 2640  
Db 2581 ATAAATAGAAATGACACAGAAAGGCTTTAAGTATCCATTGGGACATGAAGTTAAACACAGTC 2640  
Qy 2641 GGGAAACACAGCATAGAAATGGAAGAAAGTGAATTTGATGCTCAGTATTTTCAGAAATACAT 2700  
Db 2641 GGGAAACACAGCATAGAAATGGAAGAAAGTGAATTTGATGCTCAGTATTTTCAGAAATACAT 2700  
Qy 2701 TCAAGGTTTCAAAGCGCCAGTCAATTTGCTCTGTTTCAAATCCAGGAAATTCGAGAGAGG 2760  
Db 2701 TCAAGGTTTCAAAGCGCCAGTCAATTTGCTCTGTTTCAAATCCAGGAAATTCGAGAGAGG 2760  
Qy 2761 AATGTGCAACATTTCTGTGCCACTCTGGGGTCTTTAAAGAAACAAAGTCCAAAAAGTCACTT 2820  
Db 2761 AATGTGCAACATTTCTGTGCCACTCTGGGGTCTTTAAAGAAACAAAGTCCAAAAAGTCACTT 2820  
Qy 2821 TTCAATCTGAACAAAGGAGAAATCAAGGAAAGTGAATGATCTAATATCAAGCCTGTAC 2880  
Db 2821 TTCAATCTGAACAAAGGAGAAATCAAGGAAAGTGAATGATCTAATATCAAGCCTGTAC 2880  
Qy 2881 AGACAGTAAATATCACTGACGAGCTTTCTGTTGTTGTCAGAAAGATAAGCCAGTTGATA 2940  
Db 2881 AGACAGTAAATATCACTGACGAGCTTTCTGTTGTTGTCAGAAAGATAAGCCAGTTGATA 2940  
Qy 2941 ATGCCAAATGTAGTATCAAAAGGAGGCTCTAGGTTTGTCTATCATCTCAGTTCCAGAGCA 3000  
Db 2941 ATGCCAAATGTAGTATCAAAAGGAGGCTCTAGGTTTGTCTATCATCTCAGTTCCAGAGCA 3000





```

Db 5161 CTGAAGAGACTACTCATGTTGTTTATGAAGAAACAGATGCTGAGTTTGTGTGTAACGGACAC 5220
Qy 5221 TGAATATTTTCTAGGAATTCGGGAGGAAATGGGTAGTTAGTATTCTTGGGTGACCC 5280
Db 5221 TGAATATTTTCTAGGAATTCGGGAGGAAATGGGTAGTTAGTATTCTTGGGTGACCC 5280
Qy 5281 AGTCTATTAAAGAAAGAAATGCTGAATGAGCATGATTTTGAAGTCAGAGGAGATGG 5340
Db 5281 AGTCTATTAAAGAAAGAAATGCTGAATGAGCATGATTTTGAAGTCAGAGGAGATGG 5340
Qy 5341 TCAATGAGAAACCCACCAAGGTCCTCAAGCGAGCAAGAGATCCAGGACGAAAGATCT 5400
Db 5341 TCAATGAGAAACCCACCAAGGTCCTCAAGCGAGCAAGAGATCCAGGACGAAAGATCT 5400
Qy 5401 TCAGGGGCTAGAAATCTGTTGCTATGGGCCCTTCCACCAATGCCCCACAGATCAACTGG 5460
Db 5401 TCAGGGGCTAGAAATCTGTTGCTATGGGCCCTTCCACCAATGCCCCACAGATCAACTGG 5460
Qy 5461 AATGGATGGTACAGCTGTGTGCTCTTCTGTGTGAAGGAGCTTTCATCATTCACCCCTTG 5520
Db 5461 AATGGATGGTACAGCTGTGTGCTCTTCTGTGTGAAGGAGCTTTCATCATTCACCCCTTG 5520
Qy 5521 GCACAGTGTCCACCAATGTTGTTGTGTCAGCCAGATGCTGACAGAGACAATGGCT 5580
Db 5521 GCACAGTGTCCACCAATGTTGTTGTGTCAGCCAGATGCTGACAGAGACAATGGCT 5580
Qy 5581 TCCATGCAATTTGGGCAGATGTGAGGCACCTGTGTGTGACCCGAGAGTGGGTGGACA 5640
Db 5581 TCCATGCAATTTGGGCAGATGTGAGGCACCTGTGTGTGACCCGAGAGTGGGTGGACA 5640
Qy 5641 GTGTAGCACTCTACAGTGCAGGAGCTGGACACCTACCTGATACCCAGATCCCCCACA 5700
Db 5641 GTGTAGCACTCTACAGTGCAGGAGCTGGACACCTACCTGATACCCAGATCCCCCACA 5700
Qy 5701 GCCACTACTGA 5711
Db 5701 GCCACTACTGA 5711

RESULT 5
AAV46470
ID AAV46470 standard; cDNA; 5711 BP.
AC
AC
XX
XX
DT 18-NOV-1998 (first entry)
XX
XX
DE Human BRCA1 omi3 polymorphism #6 cDNA.
XX
XX
KW BRCA1; omi3; human; breast and ovarian cancer predisposing gene;
KW polymorphism; susceptibility; anti-oncogene; tumour suppressor;
KW Chromosome 17q; ss.
XX
OS Homo sapiens.
XX
XX
Key Location/Qualifiers
FH 120..5711
CD
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FT variation 4427
FT /*tag= b
FT /note= "This polymorphic variation can be a T or C
nucleotide"
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XX
US5750400-A.
XX
XX
PD 12-MAY-1998.
XX
XX
PF 12-FEB-1997; 97US-0798691.
XX
XX
PR 12-FEB-1996; 96US-0598591.
PR 12-FEB-1997; 97US-0798691.
XX
XX

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PA (ONCO-) ONCORMED INC.

XX Allen AC, Alvares CP, Critz BS, Murphy PD, Olson SJ;  
 PI Schelter DB, Zeng B;  
 XX WPI; 1998-296774/26.

DR BRCA1 omi gene coding sequences - useful for distinguishing between  
 XX polymorphisms and mutation(s) in the screening for disposition to  
 PT Breast or ovarian cancer

PS Claim 2e; Page -; 54pp; English.

XX This sequence encodes a human BRCA1 (breast and ovarian cancer  
 CC predisposing gene) omi3 gene in which a polymorphic variation occurs at  
 CC nucleotide 4427. This sequence and other polymorphic variations of this  
 CC sequence are useful for the identification of an individual who may or  
 CC may not have an increased susceptibility to breast or ovarian cancer.  
 CC The sequences used identify gene changes which are due to polymorphisms,  
 CC rather than cancer causing mutations. BRCA1 is an anti-oncogene (tumour  
 CC suppressor) which is involved in genetic inheritance of cancers,  
 CC especially breast and ovarian cancer. It is found at human chromosome  
 CC 17q which is known to be linked to cancer susceptibility, especially  
 CC breast cancer. Cells containing a mutation in this gene lose the  
 CC wild-type function of BRCA1 and are more susceptible to cancers.  
 CC NOTE: This sequence does not appear in the specification but has been  
 CC created from the wild type BRCA1 omi3 gene represented in AAV46450.

XX Sequence 5711 BP; 1953 A; 1098 C; 1277 G; 1382 T; 1 other;

Query Match 100.0%; Score 5710.6; DB 19; Length 5711;  
 Best Local Similarity 100.0%; Pred. No. 0;  
 Matches 5710; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

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DB 1381 AATATCTGTTCTTTCAGAGAAATAGACTTACTGGCCAGTGATCCTCATGAGGCTTTAA 1440  
QY 1441 TATGTAAAGTGAAGAGTTTCACTCCAAATCAGTAGAGATGAATATTGAAGACAAATAT 1500

DB 1441 TATGTAAAGTGAAGAGTTTCACTCCAAATCAGTAGAGATGAATATTGAAGACAAATAT 1500  
QY 1501 TTGGGAAAACTTATCGGAAGAGCAAGCCCTCCCAACTTTAAGCATGTAACTGAAATC 1560  
DB 1501 TTGGGAAAACTTATCGGAAGAGCAAGCCCTCCCAACTTTAAGCATGTAACTGAAATC 1560  
QY 1561 TAATTATAGGAGCATTTGTTTACTGAGCCACAGATAATACAAGAGCGTCCCTCACAATA 1620  
DB 1561 TAATTATAGGAGCATTTGTTTACTGAGCCACAGATAATACAAGAGCGTCCCTCACAATA 1620  
QY 1621 AATTAAGCGTAAAGGAGACCTACATCAGCCCTTCACTCTGAGGATTTTATCAAGAAAG 1680  
DB 1621 AATTAAGCGTAAAGGAGACCTACATCAGCCCTTCACTCTGAGGATTTTATCAAGAAAG 1680  
QY 1681 CAGATTTGGCAGTTCAAAAGACTCTCAAAATGATAAATCAGGNACTTAACCAACGGAGC 1740  
DB 1681 CAGATTTGGCAGTTCAAAAGACTCTCAAAATGATAAATCAGGNACTTAACCAACGGAGC 1740  
QY 1741 AGAATGCTCAAGTATGAATATTACTAATAGTGTGATGAGATAAATAAAGAGTGTGATT 1800  
DB 1741 AGAATGCTCAAGTATGAATATTACTAATAGTGTGATGAGATAAATAAAGAGTGTGATT 1800  
QY 1801 CTATTCAAGATGAGAAAAATCTTAACCCCAATAGAAATCACTCGAAAAAGAAATCTGCTTCA 1860  
DB 1801 CTATTCAAGATGAGAAAAATCTTAACCCCAATAGAAATCACTCGAAAAAGAAATCTGCTTCA 1860  
QY 1861 AAAGAAAGCTGAACCTTAAAGCAGGATATAGCAATATGGAATCGAATTAATATCTC 1920  
DB 1861 AAAGAAAGCTGAACCTTAAAGCAGGATATAGCAATATGGAATCGAATTAATATCTC 1920  
QY 1921 ACAATTCAAAAGCACCCTAAAAGAAATAGGCTGAGGAGAAAGTCTTTACCAAGGATATTC 1980  
DB 1921 ACAATTCAAAAGCACCCTAAAAGAAATAGGCTGAGGAGAAAGTCTTTACCAAGGATATTC 1980  
QY 1981 ATGCGCTTGAACCTAGTAGTACAGTAGAAATCTAAGCCCACTAATTTGTAATGCAAA 2040  
DB 1981 ATGCGCTTGAACCTAGTAGTACAGTAGAAATCTAAGCCCACTAATTTGTAATGCAAA 2040  
QY 2041 TTGATAGTTGTTCTAGCAGTGAAGAGTAAGAAAAAGTACAAATGCGAGTCA 2100  
DB 2041 TTGATAGTTGTTCTAGCAGTGAAGAGTAAGAAAAAGTACAAATGCGAGTCA 2100  
QY 2101 GGACACAGCAAACTTACAACTCATGGAAGTAAAGAACTGCACTGGAAGCCAAAGAA 2160  
DB 2101 GGACACAGCAAACTTACAACTCATGGAAGTAAAGAACTGCACTGGAAGCCAAAGAA 2160  
QY 2161 GTAAACAGCCAAATGAAACAGCAAGTAAAGACATGACAGYGATCTTTCCAGAGCTGA 2220  
DB 2161 GTAAACAGCCAAATGAAACAGCAAGTAAAGACATGACAGYGATCTTTCCAGAGCTGA 2220  
QY 2221 AGTTACAAATGCACTGGTTCTTTTACTAAGTGTTCAAATACCAAGTGAAGTAAAGAT 2280  
DB 2221 AGTTACAAATGCACTGGTTCTTTTACTAAGTGTTCAAATACCAAGTGAAGTAAAGAT 2280  
QY 2281 TTGTCAATCTAGCTTCCAAAGAGAAAGAAAGAGAACTAGAAACAGTTTAAAGTGT 2340  
DB 2281 TTGTCAATCTAGCTTCCAAAGAGAAAGAAAGAGAACTAGAAACAGTTTAAAGTGT 2340  
QY 2341 CTAATATGCTGAAGACCCCAAGATCTCATGTTAAGTGGAGAAAGGTTTTCGAAACTG 2400  
DB 2341 CTAATATGCTGAAGACCCCAAGATCTCATGTTAAGTGGAGAAAGGTTTTCGAAACTG 2400  
QY 2401 AAAGATCTGAGAGATGAGCATTTTCACTGGTACTGCTGATGATGAGGACTCAGG 2460  
DB 2401 AAAGATCTGAGAGATGAGCATTTTCACTGGTACTGCTGATGATGAGGACTCAGG 2460  
QY 2461 AAAGTATCTGTTTACTGGAAGTGTAGCACTCTAGGGAAGGCAAAACAGAACTAAAT 2520  
DB 2461 AAAGTATCTGTTTACTGGAAGTGTAGCACTCTAGGGAAGGCAAAACAGAACTAAAT 2520  
QY 2521 GTGTGATGCTAGTGTGACGATTTTGAACCCCAAGGAGTAAATTCATGTTGTTTCCAAAG 2580





Qy	4741	AGTCTGGGCCACACGATTTGACGAAACATCTTACTTTCGCCAAGCAAGATCTAGAGGAA	4800
Db	4741	AGTCTGGGCCACACGATTTGACGAAACATCTTACTTTCGCCAAGCAAGATCTAGAGGAA	4800
Qy	4801	CCCCTTACTGGAATCTGGAAATCAGCCTCTTCTCTGATGACCCCTGAATCTGATCTCTTCTG	4860
Db	4801	CCCCTTACTGGAATCTGGAAATCAGCCTCTTCTCTGATGACCCCTGAATCTGATCTCTTCTG	4860
Qy	4861	AAGACAGAGCCCAGAGTCAGCTCGTGTGTGGCAAATACCACATCTTCAACCTCTGCATTGA	4920
Db	4861	AAGACAGAGCCCAGAGTCAGCTCGTGTGTGGCAAATACCACATCTTCAACCTCTGCATTGA	4920
Qy	4921	AAGTTCCGCAATTCGAAAGTTGACAGAACTGCCCHCAGGGTCGAGCTGCTCATACTACTG	4980
Db	4921	AAGTTCCGCAATTCGAAAGTTGACAGAACTGCCCHCAGGGTCGAGCTGCTCATACTACTG	4980
Qy	4981	ATACTGCTGGGTATAATTCGCAATGAAGAAAGTGTGACAGGGAGAACCCAGAATTGACAG	5040
Db	4981	ATACTGCTGGGTATAATTCGCAATGAAGAAAGTGTGACAGGGAGAACCCAGAATTGACAG	5040
Qy	5041	CTTCAAACAGAAAGGTCACAAAAAGATTCCTAGTGGTGTCTGGGCTGACCCCGAAG	5100
Db	5041	CTTCAAACAGAAAGGTCACAAAAAGATTCCTAGTGGTGTCTGGGCTGACCCCGAAG	5100
Qy	5101	AATTTATGTCGTGTACAAAGTTTCCAGAAAACACACATCACTTTAACTAATTA	5160
Db	5101	AATTTATGTCGTGTACAAAGTTTCCAGAAAACACACATCACTTTAACTAATTA	5160
Qy	5161	CTGAAGAGACTACTCATCTGTTGTTATGAAAAACAGATGCTGAGTTTGTGTGAAACGACAC	5220
Db	5161	CTGAAGAGACTACTCATCTGTTGTTATGAAAAACAGATGCTGAGTTTGTGTGAAACGACAC	5220
Qy	5221	TGAAATATTTTCTAGGAATTCGCGGAGGAAAAATGGGTAGTTAGCTATTTCTGGGTGACCC	5280
Db	5221	TGAAATATTTTCTAGGAATTCGCGGAGGAAAAATGGGTAGTTAGCTATTTCTGGGTGACCC	5280
Qy	5281	AGTCTATTAAAGAAAGAAAAATGCTGAAATGAGCATGATTTTGAAGTCAGAGGAGATGTGG	5340
Db	5281	AGTCTATTAAAGAAAGAAAAATGCTGAAATGAGCATGATTTTGAAGTCAGAGGAGATGTGG	5340
Qy	5341	TCAATGAAGAAACCCCAAGGTCCTGAAAGCGAGCAAGAGAAATCCAGGACAGAAAGATCT	5400
Db	5341	TCAATGAAGAAACCCCAAGGTCCTGAAAGCGAGCAAGAGAAATCCAGGACAGAAAGATCT	5400
Qy	5401	TCAGGGGCTAGAAATCTGTTGCTATCGGCGCCTTCAACAATGCCACAGATCAACTGG	5460
Db	5401	TCAGGGGCTAGAAATCTGTTGCTATCGGCGCCTTCAACAATGCCACAGATCAACTGG	5460
Qy	5461	AATGGATGTACAGCTGTGTGGTGCTTCTGTGGTGAAGGAGCTTTTCATCAATTCACCCCTTG	5520
Db	5461	AATGGATGTACAGCTGTGTGGTGCTTCTGTGGTGAAGGAGCTTTTCATCAATTCACCCCTTG	5520
Qy	5521	GCAAGGTGTCCACCCCAATTTGGTTGTGCGCCAGATGCGCTGAGAGGACAAATGGCT	5580
Db	5521	GCAAGGTGTCCACCCCAATTTGGTTGTGCGCCAGATGCGCTGAGAGGACAAATGGCT	5580
Qy	5581	TCCATGCAATTTGGGCAATGTGTGAGGCACTGTGTGTGAACCGAGAGTGGGTGTGGACA	5640
Db	5581	TCCATGCAATTTGGGCAATGTGTGAGGCACTGTGTGTGAACCGAGAGTGGGTGTGGACA	5640
Qy	5641	GTGTAGCACTCTACAGTGGCCAGAGCTGGACACACTTACCTGATACCCAGATCCCCACA	5700
Db	5641	GTGTAGCACTCTACAGTGGCCAGAGCTGGACACACTTACCTGATACCCAGATCCCCACA	5700
Qy	5701	GCCACTACTGA	5711
Db	5701	GCCACTACTGA	5711

RESULT 7

RESULI /  
AAV46452

AAV46452  
ID AAV46452 standard; cDNA; 5711 BP.

XX

AC AAV46452;

XX 18-NOV-1998 (first entry)

XX Human BRCA1 omil polymorphism #2 cDNA.

DE BRCA1; omil; human; breast and ovarian cancer predisposing gene;

XX polymorphism; susceptibility; anti-oncogene; tumour suppressor;

KW chromosome 17q; ss.

XX

OS Homo sapiens.

XX

XX Key Location/Qualifiers

FT CDS 120..5711

FT FT /\*tag= a

FT FT /product= "BRCA1 omil protein"

FT FT 2430

FT FT /\*tag= b

FT FT /note= "This polymorphic variation can be a T or C nucleotide"

XX

XX US5750400-A.

XX

XX 12-MAY-1998.

XX

XX 12-FEB-1997; 97US-0798691.

XX

XX 12-FEB-1996; 96US-0598591.

PR 12-FEB-1997; 97US-0798691.

XX

XX (ONCO-) ONCORMED INC.

XX

XX Allen AC, Alvares CP, Critz BS, Murphy PD, Olson SJ;

PI Schelter DB, Zeng B;

XX

XX WPI; 1998-296774/26.

XX

XX BRCA1 omi gene coding sequences - useful for distinguishing between

PT polymorphisms and mutation(s) in the screening for disposition to

PT breast or ovarian cancer

XX

XX Claim 2e; Page -; 54pp; English.

XX

XX This sequence encodes a human BRCA1 (breast and ovarian cancer

CC predisposing gene) omil gene in which a polymorphic variation occur

CC nucleotide 2430. This sequence and other polymorphic variations of

CC sequence are useful for the identification of an individual who

CC may not have an increased susceptibility to breast or ovarian cancer

CC The sequences used identify gene changes which are due to polymorph

CC rather than cancer causing mutations. BRCA1 is an anti-oncogene (t

CC suppressor) which is involved in genetic inheritance of cancers,

CC especially breast and ovarian cancer. It is found at human chromos

CC 17q which is known to be linked to cancer susceptibility, especial

CC breast cancer. Cells containing a mutation in this gene lose the

CC wild-type function of BRCA1 and are more susceptible to cancers.

CC NOTE: This sequence does not appear in the specification but has b

CC created from the wild type BRCA1 omil gene represented in AAV46448

XX

XX Sequence 5711 BP; 1953 A; 1098 C; 1277 G; 1382 T; 1 other;

XX

RESULT 7

RESULI /  
AAV46452

AAV46452  
ID AAV46452 standard; cDNA; 5711 BP.

XX

Db 121 TGGATTTATCTGCTCTTCGCGTTGAAGAAGTACAAAATGTCAATTAATGCTATGCATGCAGAAAA 180  
Qy 181 TCTTAGAGTGCCCATCTGTCTGGAGTTGATCAAGGAACCTGTCTCCACAAAGTGTGACC 240  
Db 181 TCTTAGAGTGCCCATCTGTCTGGAGTTGATCAAGGAACCTGTCTCCACAAAGTGTGACC 240  
Qy 241 ACATATTTGGCAAAATTTTGGATGCTGAAAATCTTCTCAACAGAGAAAGGGGCTTCAAGT 300  
Db 241 ACATATTTGGCAAAATTTTGGATGCTGAAAATCTTCTCAACAGAGAAAGGGGCTTCAAGT 300  
Qy 301 GTCCCTTATGTAAGATGATATACCAAAAGGAGCTACAGAAAGTACAGAGATTTAGTC 360  
Db 301 GTCCCTTATGTAAGATGATATACCAAAAGGAGCTACAGAAAGTACAGAGATTTAGTC 360  
Qy 361 AACTTGTGTGAAGAGCTATTTGAAAATCAATTTGTGCTTTTTCAGCTTGGACACAGATTTGGAGT 420  
Db 361 AACTTGTGTGAAGAGCTATTTGAAAATCAATTTGTGCTTTTTCAGCTTGGACACAGATTTGGAGT 420  
Qy 421 ATGCAAAACAGCTATAATTTTGCAGAAAAGGAAAATAACTCTCTGAAACATCTAAAAGATG 480  
Db 421 ATGCAAAACAGCTATAATTTTGCAGAAAAGGAAAATAACTCTCTGAAACATCTAAAAGATG 480  
Qy 481 AAGTTTCTATCATCCAAAGTATGGCTACAGAAACCGTGCCAAAAGACTTCTACAGAGTG 540  
Db 481 AAGTTTCTATCATCCAAAGTATGGCTACAGAAACCGTGCCAAAAGACTTCTACAGAGTG 540  
Qy 541 AACCAGAAAATCTCTTCTGAGGAAACCGAGTCTCAGTGTCCAACTCTCTAACCTTGGAA 600  
Db 541 AACCAGAAAATCTCTTCTGAGGAAACCGAGTCTCAGTGTCCAACTCTCTAACCTTGGAA 600  
Qy 601 CTGTGAGAACTCTGAGGACAAAGCAGCGGATACAACTCTCAAAAGACGCTGTCTACATTG 660  
Db 601 CTGTGAGAACTCTGAGGACAAAGCAGCGGATACAACTCTCAAAAGACGCTGTCTACATTG 660  
Qy 661 AATTGGGATCTGATCTCTGAAAGTACCGTTAATAGGCAACTTATTTGCAAGTGTGGAG 720  
Db 661 AATTGGGATCTGATCTCTGAAAGTACCGTTAATAGGCAACTTATTTGCAAGTGTGGAG 720  
Qy 721 ATCAAGAAATCTTACAAATCAACCTCAAGGAAACGAGGATGAAATCAGTTTGGATCTG 780  
Db 721 ATCAAGAAATCTTACAAATCAACCTCAAGGAAACGAGGATGAAATCAGTTTGGATCTG 780  
Qy 781 CAAAAAGGCTGCTGTGAAATTTTCTGAGACGGATGTAAACAAATCTGAAACATCATCAAC 840  
Db 781 CAAAAAGGCTGCTGTGAAATTTTCTGAGACGGATGTAAACAAATCTGAAACATCATCAAC 840  
Qy 841 CCAGTAAATATGATTTGAAACCACTGAGAAAGCGTGCGCTGAGAGGATCCAGAAAGT 900  
Db 841 CCAGTAAATATGATTTGAAACCACTGAGAAAGCGTGCGCTGAGAGGATCCAGAAAGT 900  
Qy 901 ATCAGGGTAGTTCTGTTTCAAACTTGCATGTGGAGCCATGTGGCACAATACTCATGCCA 960  
Db 901 ATCAGGGTAGTTCTGTTTCAAACTTGCATGTGGAGCCATGTGGCACAATACTCATGCCA 960  
Qy 961 GCTCATTTACAGCATGAGAAACAGCAGTTTATTTACTTCACTTAAGACAGAAATGTAGAAA 1020  
Db 961 GCTCATTTACAGCATGAGAAACAGCAGTTTATTTACTTCACTTAAGACAGAAATGTAGAAA 1020  
Qy 1021 AGGCTGAATTTCTGTAATAAAGCAAAACAGCTGTGCTTAGAAGGAGCCAAACATTAACAGAT 1080  
Db 1021 AGGCTGAATTTCTGTAATAAAGCAAAACAGCTGTGCTTAGAAGGAGCCAAACATTAACAGAT 1080  
Qy 1081 GGGCTGGAAGTAAAGAAACATGTAATGATAGCGGACTCCAGCAGCAAGAAAAGGTAG 1140  
Db 1081 GGGCTGGAAGTAAAGAAACATGTAATGATAGCGGACTCCAGCAGCAAGAAAAGGTAG 1140  
Qy 1141 ATCTGAATGCTGATCCCTGTGTGAGAAAAGAAATGGAATAAGCAGAAAACCTGCCATGCT 1200  
Db 1141 ATCTGAATGCTGATCCCTGTGTGAGAAAAGAAATGGAATAAGCAGAAAACCTGCCATGCT 1200  
Qy 1201 CAGAGAAATCTTAGAGATATCTGAAGATGTTCTTGGATAACTAATAATAGCAGCAATTCAGA 1260

Db 1201 CAGAGAAATCTTAGAGATATCTGAAGATGTTCTCTGGATAAACACTAAATAGCAGCAATTCAGA 1260  
Qy 1261 AAGTTAAATGAGTGGTTTTTCCAGAAAGTGAATGAATGTTTAGGTTCTTGATGACTCACATGATG 1320  
Db 1261 AAGTTAAATGAGTGGTTTTTCCAGAAAGTGAATGAATGTTTAGGTTCTTGATGACTCACATGATG 1320  
Qy 1321 GGGAGTCTGAATCAAAATGCCAAAGTAGCTGATGATTTGGAGCTTCTAAATGAGGTAGATG 1380  
Db 1321 GGGAGTCTGAATCAAAATGCCAAAGTAGCTGATGATTTGGAGCTTCTAAATGAGGTAGATG 1380  
Qy 1381 AATATTTCTGTTCTTTCAGAGAAAATAGACTTACTTGGCCAGTGATCTCTCATGAGGCTTTAA 1440  
Db 1381 AATATTTCTGTTCTTTCAGAGAAAATAGACTTACTTGGCCAGTGATCTCTCATGAGGCTTTAA 1440  
Qy 1441 TATGTAAAGTGAAGAGTTTCACTCCAAATCAGTAGAGAGTAATATTTGAAGACAAAATAT 1500  
Db 1441 TATGTAAAGTGAAGAGTTTCACTCCAAATCAGTAGAGAGTAATATTTGAAGACAAAATAT 1500  
Qy 1501 TTGGGAAAACTTATCGGAAGAGGCAAGCCCTCCCAACTTTAAGCCATGTAACTGAAAATC 1560  
Db 1501 TTGGGAAAACTTATCGGAAGAGGCAAGCCCTCCCAACTTTAAGCCATGTAACTGAAAATC 1560  
Qy 1561 TAAATTTAGGAGCAATTTGTTTACTTGAGCCACAGATAAATACAAGAGCGTCCCTCACAATA 1620  
Db 1561 TAAATTTAGGAGCAATTTGTTTACTTGAGCCACAGATAAATACAAGAGCGTCCCTCACAATA 1620  
Qy 1621 AATTTAAAGCGTAAAGAGAGACTTACATCAGCGCTTCTCTGAGGATTTTATCAAGAAAG 1680  
Db 1621 AATTTAAAGCGTAAAGAGAGACTTACATCAGCGCTTCTCTGAGGATTTTATCAAGAAAG 1680  
Qy 1681 CAGATTTGGCAGTTTCAAAAGACTCTCTGAAATGATTAATCAGGGAACTAAACAAACGGAGC 1740  
Db 1681 CAGATTTGGCAGTTTCAAAAGACTCTCTGAAATGATTAATCAGGGAACTAAACAAACGGAGC 1740  
Qy 1741 AGAATGCTCAAGTGAATTAATTTACTTAATAGTGTCTAGAGATAAACAAGAGTGAAT 1800  
Db 1741 AGAATGCTCAAGTGAATTAATTTACTTAATAGTGTCTAGAGATAAACAAGAGTGAAT 1800  
Qy 1801 CTATTTCAAGATGAGAAAAATCTTAAACCAATAGAAATCACTCGAAAAAGAAATCTGCTTTCA 1860  
Db 1801 CTATTTCAAGATGAGAAAAATCTTAAACCAATAGAAATCACTCGAAAAAGAAATCTGCTTTCA 1860  
Qy 1861 AAACGAAAGCTGAACCTTATTAAGCAGCAGTATTAAGCAATATGGAACCTCGAATTAATAATCC 1920  
Db 1861 AAACGAAAGCTGAACCTTATTAAGCAGCAGTATTAAGCAATATGGAACCTCGAATTAATAATCC 1920  
Qy 1921 ACAATTCAGAAAGCACTTAAAGAAAGTATGGCTGAGGAGGAAAGTCTTCTACCCAGGCATATTC 1980  
Db 1921 ACAATTCAGAAAGCACTTAAAGAAAGTATGGCTGAGGAGGAAAGTCTTCTACCCAGGCATATTC 1980  
Qy 1981 ATGGCTTGAACCTAGTAGTCACTAGAAATCTTAAGCCCACTTAATTTGTACTGAAATTCGAAA 2040  
Db 1981 ATGGCTTGAACCTAGTAGTCACTAGAAATCTTAAGCCCACTTAATTTGTACTGAAATTCGAAA 2040  
Qy 2041 TTGATAGTGTCTTTCAGAGTGAAGAGATAAAGAAAAAGTACAACCAAAATGCCAGTCA 2100  
Db 2041 TTGATAGTGTCTTTCAGAGTGAAGAGATAAAGAAAAAGTACAACCAAAATGCCAGTCA 2100  
Qy 2101 GGCAACAGAAAACCTTCAACTCATGGAAGTAAAGAACCTGCAACTGGAGGCCAAGAGA 2160  
Db 2101 GGCAACAGAAAACCTTCAACTCATGGAAGTAAAGAACCTGCAACTGGAGGCCAAGAGA 2160  
Qy 2161 GTAAACAGCCAAATGAACAGACAGTAAAGACATGACAGTGATATTTCCAGAGCTGA 2220  
Db 2161 GTAAACAGCCAAATGAACAGACAGTAAAGACATGACAGTGATATTTCCAGAGCTGA 2220  
Qy 2221 AGTTAAACAAATGCAACCTGTTCTTTTACTAAGTGTTCAAATACCAGTGAACCTTAAAGAAAT 2280  
Db 2221 AGTTAAACAAATGCAACCTGTTCTTTTACTAAGTGTTCAAATACCAGTGAACCTTAAAGAAAT 2280  
Qy 2281 TTGTCAATCTTAGCCCTTCCAGAGAGAAAAGAGAAACTAGAAACAGTAAAGTGT 2340  
Db 2281 TTGTCAATCTTAGCCCTTCCAGAGAGAAAAGAGAAACTAGAAACAGTAAAGTGT 2340

QY 2341 CTAATAATGCTGAAGACCCCAAGATCTCATGTTAAGTGAAGAAAGGGTGTTCGAAACTG 2400  
DB 2341 CTAATAATGCTGAAGACCCCAAGATCTCATGTTAAGTGAAGAAAGGGTGTTCGAAACTG 2400  
QY 2401 AAAGATCTGTAGAGTAGCAGTAGTATTTCACTGGTACCTGGTACTGATTTATGGCACTCAGG 2460  
DB 2401 AAAGATCTGTAGAGTAGCAGTAGTATTTCACTGGTACTGATTTATGGCACTCAGG 2460  
QY 2461 AAAGTATCTGTTACTGGAAGTTAGCACTCTAGGGAAGGCAAAAACAGAACCAATAAAT 2520  
DB 2461 AAAGTATCTGTTACTGGAAGTTAGCACTCTAGGGAAGGCAAAAACAGAACCAATAAAT 2520  
QY 2521 GTGTGAGTCAGTGTGACGATTTGCAAAACCCCAAGGACATAATTCATGGTGTTCGAAAG 2580  
DB 2521 GTGTGAGTCAGTGTGACGATTTGCAAAACCCCAAGGACATAATTCATGGTGTTCGAAAG 2580  
QY 2581 ATAATAGAAATGACACAGAAAGGCTTTAAGTATCCATTTGGGACATGAAGTTAAACACAGTC 2640  
DB 2581 ATAATAGAAATGACACAGAAAGGCTTTAAGTATCCATTTGGGACATGAAGTTAAACACAGTC 2640  
QY 2641 GGGAAACAGCATAGAAATGGAAGAAAGTGAACCTTGATGCTCAGTATTTGAGAAATACAT 2700  
DB 2641 GGGAAACAGCATAGAAATGGAAGAAAGTGAACCTTGATGCTCAGTATTTGAGAAATACAT 2700  
QY 2701 TCAAGGTTTCAAAGCGCCAGTCATTTGCTCTGTTTTCAAAATCCAGGAAATGCGAAGAGG 2760  
DB 2701 TCAAGGTTTCAAAGCGCCAGTCATTTGCTCTGTTTTCAAAATCCAGGAAATGCGAAGAGG 2760  
QY 2761 AATGTGCAACATCTCTGCCCCACTCTGGTCTTTAAAGAAACAAAGTCCAAAAGTCACTT 2820  
DB 2761 AATGTGCAACATCTCTGCCCCACTCTGGTCTTTAAAGAAACAAAGTCCAAAAGTCACTT 2820  
QY 2821 TTGAATGTGAACAAAGGAGAAATCAAGAAAGAAATGAGTCTTAATATCAAGCCTGTAC 2880  
DB 2821 TTGAATGTGAACAAAGGAGAAATCAAGAAAGAAATGAGTCTTAATATCAAGCCTGTAC 2880  
QY 2881 AGACAGTAAATATCACTGCAAGGCTTTCTGCTGGTGTGTCAGAAAGATAAGCCAGTTCATA 2940  
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QY 2941 ATGCCAAATGAGTATCAAAAGGAGGCTCTAGGTTTTGCTATCATCTCAGTTCAGAGGCA 3000  
DB 2941 ATGCCAAATGAGTATCAAAAGGAGGCTCTAGGTTTTGCTATCATCTCAGTTCAGAGGCA 3000  
QY 3001 ACGAACTGGACTCATTTACTCCAAATAAACATGCACTTTTACAAAACCCATATCGTATAC 3060  
DB 3001 ACGAACTGGACTCATTTACTCCAAATAAACATGCACTTTTACAAAACCCATATCGTATAC 3060  
QY 3061 CACCACCTTTTCCCATCAAGTCATTTGTTAAACCTAAATGTAAGAAAAATCTGCTAGAGG 3120  
DB 3061 CACCACCTTTTCCCATCAAGTCATTTGTTAAACCTAAATGTAAGAAAAATCTGCTAGAGG 3120  
QY 3121 AAAAATTTGAGGAAATCAATGTCACCTGAAGAGAAATGGGAAATGAGAAATTCCAA 3180  
DB 3121 AAAAATTTGAGGAAATCAATGTCACCTGAAGAGAAATGGGAAATGAGAAATTCCAA 3180  
QY 3181 GTACAGTGACACAAATTAGCCGTAAATCAATTAGAGAAATGTTTTTAAAGGAGCCAGCT 3240  
DB 3181 GTACAGTGACACAAATTAGCCGTAAATCAATTAGAGAAATGTTTTTAAAGGAGCCAGCT 3240  
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DB 3241 CAAGCAATATTAATGAAGTAGGTTCCAGTAGTAAATGAAGTGGGCTCCAGTATTAATGAAA 3300  
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DB 3301 TAGGTTCCAGTGATGAAAAATCAAGCAGAACTAGGTAGAAAACAGAGGCGCAAAATTTGA 3360  
QY 3361 ATGCTATGCTTAGATTAGGGGTTTTGCAACCTGAGGCTTATTAACAAAGCTTTCCTGGAA 3420  
DB 3361 ATGCTATGCTTAGATTAGGGGTTTTGCAACCTGAGGCTTATTAACAAAGCTTTCCTGGAA 3420

QY 3421 GTAAATGTAAGATCCTGAAATAAAAAGCAAGAAATATGAAGAAAGTAGTTTCAGACTGTTA 3480  
DB 3421 GTAAATGTAAGATCCTGAAATAAAAAGCAAGAAATATGAAGAAAGTAGTTTCAGACTGTTA 3480  
QY 3481 ATACAGATTTTCTCTCCATATCTGATTTTCAGATAACTTTAGAACAGCCTATGGGAAGTAGTC 3540  
DB 3481 ATACAGATTTTCTCTCCATATCTGATTTTCAGATAACTTTAGAACAGCCTATGGGAAGTAGTC 3540  
QY 3541 ATGCATCTCAGGTTTGTCTGAGACACCTGATGACCTGTTAGATGATGGTGAATAAAGG 3600  
DB 3541 ATGCATCTCAGGTTTGTCTGAGACACCTGATGACCTGTTAGATGATGGTGAATAAAGG 3600  
QY 3601 AAGATCTAGTCTTGTCTGAAAAATGACATTAAGGAAAGCTCTGCTGTTTTTAGCAAAAGCG 3660  
DB 3601 AAGATCTAGTCTTGTCTGAAAAATGACATTAAGGAAAGCTCTGCTGTTTTTAGCAAAAGCG 3660  
QY 3661 TCCAGAGAGGAGAGCTTTAGCAGGAGTCTTAGCCCTTTCAACCCTATACACATTTGGCTCAGG 3720  
DB 3661 TCCAGAGAGGAGAGCTTTAGCAGGAGTCTTAGCCCTTTCAACCCTATACACATTTGGCTCAGG 3720  
QY 3721 GTTACCGAAGAGGGGCCAAGAAATTAGAGTCTCTCAGAAAGAACTTATCTAGTGAGGATG 3780  
DB 3721 GTTACCGAAGAGGGGCCAAGAAATTAGAGTCTCTCAGAAAGAACTTATCTAGTGAGGATG 3780  
QY 3781 AAGAGCTTCCCTGCTTCCAAACACTTTGTTATTTGGTAAAGTAAACAAATATACCTTCTCAGT 3840  
DB 3781 AAGAGCTTCCCTGCTTCCAAACACTTTGTTATTTGGTAAAGTAAACAAATATACCTTCTCAGT 3840  
QY 3841 CTACTAGGCATAGCACCGTTGCTTACCGAGTGTCTGCTTAAGAAACACAGAGGAGAAATTTAT 3900  
DB 3841 CTACTAGGCATAGCACCGTTGCTTACCGAGTGTCTGCTTAAGAAACACAGAGGAGAAATTTAT 3900  
QY 3901 TATCATTTGAAGAAATAGCTTAAATGACTGCAAGTAAACAGGTAATTTGSCAAAGGATCTC 3960  
DB 3901 TATCATTTGAAGAAATAGCTTAAATGACTGCAAGTAAACAGGTAATTTGSCAAAGGATCTC 3960  
QY 3961 AGGAAACATCACTTAGTGAGGAAACAAAATGTTCTGCTAGCTTGTGTTTTTTCACAGTGCA 4020  
DB 3961 AGGAAACATCACTTAGTGAGGAAACAAAATGTTCTGCTAGCTTGTGTTTTTTCACAGTGCA 4020  
QY 4021 GTGAAATTTGGAAGACTTGACTGCAAAATACAAACCCAGGATCCTTTCTGATTTGGTTCTT 4080  
DB 4021 GTGAAATTTGGAAGACTTGACTGCAAAATACAAACCCAGGATCCTTTCTGATTTGGTTCTT 4080  
QY 4081 CCAACAAATGAGGCACTCAGTCTGAAAGCCAGGAGTTGCTCTGAGTGACAAAGAAATTTGG 4140  
DB 4081 CCAACAAATGAGGCACTCAGTCTGAAAGCCAGGAGTTGCTCTGAGTGACAAAGAAATTTGG 4140  
QY 4141 TTTTCAGATGATGAAGAAAGAGGAAACGGGCTTTGGAAGAAAATAATCAAGAAAGAGCAAGCA 4200  
DB 4141 TTTTCAGATGATGAAGAAAGAGGAAACGGGCTTTGGAAGAAAATAATCAAGAAAGAGCAAGCA 4200  
QY 4201 TGGATTCAAACTTAGGTGAAGCAGCATCTGGGTGTGAGAGTGAAACAAAGCGTCTCTGAAG 4260  
DB 4201 TGGATTCAAACTTAGGTGAAGCAGCATCTGGGTGTGAGAGTGAAACAAAGCGTCTCTGAAG 4260  
QY 4261 ACTGCTCAGGGCTATCCTCTCAGAGTGACATTTTAAACCACTCAGCAGAGGATACCAATGC 4320  
DB 4261 ACTGCTCAGGGCTATCCTCTCAGAGTGACATTTTAAACCACTCAGCAGAGGATACCAATGC 4320  
QY 4321 AACATAACCTGATAAAAGCTCCAGCAGGAAATGGCTGAACCTAGAAAGCTGTGTAGAAACAGC 4380  
DB 4321 AACATAACCTGATAAAAGCTCCAGCAGGAAATGGCTGAACCTAGAAAGCTGTGTAGAAACAGC 4380  
QY 4381 ATGGGAGCCAGCCTTCTAAACAGTACCCCTTCCATCAATAGTGACTCTCTGCTGCCCTTGAAG 4440  
DB 4381 ATGGGAGCCAGCCTTCTAAACAGTACCCCTTCCATCAATAGTGACTCTCTGCTGCCCTTGAAG 4440  
QY 4441 ACCTGCGAATTCAGAACAGCAGATCAGAAAAGCAGTATTAACTTCACAGAAAGTA 4500  
DB 4441 ACCTGCGAATTCAGAACAGCAGATCAGAAAAGCAGTATTAACTTCACAGAAAGTA 4500  
QY 4501 GTGAATACCCCTATAAGCCAGAAATCCAGAAAGGCCCTTTCTGCTGACAAAGTTTGGAGTGCTG 4560



SQ Sequence 5711 BP; 1953 A; 1099 C; 1277 G; 1381 T; 1 other;									
Query Match 100.0%; Score 5710.6; DB 19; Length 5711;									
Best Local Similarity 100.0%; Pred. No. 0;									
Matches 5710; Conservative 1; Mismatches 0; Indels 0; Gaps 0;									
Qy	1	AGCTCGCTGAGACTTCCTGGACCCCGCACAGGCTGTGGGTTTCTCAGATAA	CTGGGCC	60					
Db	1	AGCTCGCTGAGACTTCCTGGACCCCGCACAGGCTGTGGGTTTCTCAGATAA	CTGGGCC	60					
Qy	61	CTGGGCTCAGAGGCTTCAACCTCTGCTCTGGGTAAAGTTCATGGAACAGAA	AA	120					
Db	61	CTGGGCTCAGAGGCTTCAACCTCTGCTCTGGGTAAAGTTCATGGAACAGAA	AA	120					
Qy	121	TGGATTATCTGCTCTGCGCTGGAAGTACAAATGTCAATTAAGTCTATGAGAA	AA	180					
Db	121	TGGATTATCTGCTCTGCGCTGGAAGTACAAATGTCAATTAAGTCTATGAGAA	AA	180					
Qy	181	TCCTAGAGTGTCCCATCTGCTGGAGTTGATCAAGGAACCTGTCTCCACAAAGT	GTGACC	240					
Db	181	TCCTAGAGTGTCCCATCTGCTGGAGTTGATCAAGGAACCTGTCTCCACAAAGT	GTGACC	240					
Qy	241	ACATATTTTGCATAATTTTGCATGCTGAACTTCTCAACCAAGAGGGCTTCA	CAGT	300					
Db	241	ACATATTTTGCATAATTTTGCATGCTGAACTTCTCAACCAAGAGGGCTTCA	CAGT	300					
Qy	301	GTCCCTTATGTAAGATGATATACCAAAAGGACCTACAGAAAGTACGAGATT	TAGT	360					
Db	301	GTCCCTTATGTAAGATGATATACCAAAAGGACCTACAGAAAGTACGAGATT	TAGT	360					
Qy	361	AACCTGTTGAAGAGCTATTTGAAATCAATTTGTGCTTTTACGCTTGACAC	AGTTTGAGT	420					
Db	361	AACCTGTTGAAGAGCTATTTGAAATCAATTTGTGCTTTTACGCTTGACAC	AGTTTGAGT	420					
Qy	421	ATGCAAAACAGCTATAATTTTGCRAAAAAGGAAATAACTCTCTGAAACAT	CTAAAGATG	480					
Db	421	ATGCAAAACAGCTATAATTTTGCRAAAAAGGAAATAACTCTCTGAAACAT	CTAAAGATG	480					
Qy	481	AAGTTTCTATCATCAAGATATGGCTACAGAAACCGTCCCAAGACTTCTA	CAGAGTG	540					
Db	481	AAGTTTCTATCATCAAGATATGGCTACAGAAACCGTCCCAAGACTTCTA	CAGAGTG	540					
Qy	541	AACCCGAAATTCCTTCTGAGGAAACCACTCTCAGTGTCCAATCTCTAAC	CTTGAA	600					
Db	541	AACCCGAAATTCCTTCTGAGGAAACCACTCTCAGTGTCCAATCTCTAAC	CTTGAA	600					
Qy	601	CTGTGAGAACTCTGAGGACAAAGCAGCGGATACAACTCAAAAGACGCT	GTCTACATTG	660					
Db	601	CTGTGAGAACTCTGAGGACAAAGCAGCGGATACAACTCAAAAGACGCT	GTCTACATTG	660					
Qy	661	AATTGGGATCTGATTTCTCAAGATACCGTTAATAGGCAACTTATTGCA	GTGGGAG	720					
Db	661	AATTGGGATCTGATTTCTCAAGATACCGTTAATAGGCAACTTATTGCA	GTGGGAG	720					
Qy	721	ATCAAGAAATTTTACAATCACCCCTCAAGAACCCAGGATGAAATCAGT	TTTGATTCTG	780					
Db	721	ATCAAGAAATTTTACAATCACCCCTCAAGAACCCAGGATGAAATCAGT	TTTGATTCTG	780					
Qy	781	CAAAAAAGGCTGTGTAATTTTCTGAGCGGATGAAACAAATCTGAA	CATCAAC	840					
Db	781	CAAAAAAGGCTGTGTAATTTTCTGAGCGGATGAAACAAATCTGAA	CATCAAC	840					
Qy	841	CCAGTAATATGATTTGAAACCACTGAGAGCGTGTGAGGACATCCAGA	AAAGT	900					
Db	841	CCAGTAATATGATTTGAAACCACTGAGAGCGTGTGAGGACATCCAGA	AAAGT	900					
Qy	901	ATCAGGCTAGTTCGTGTTTCAAACTTGATGTGGAGCCATGTGGCACA	AAATCTCATGCCA	960					
Db	901	ATCAGGCTAGTTCGTGTTTCAAACTTGATGTGGAGCCATGTGGCACA	AAATCTCATGCCA	960					
Qy	961	GCTCATTACAGCATGAGAACAGCAGTTTATTACTCTCTAAAGACAGA	ATGATGAGAA	1020					
Db	961	GCTCATTACAGCATGAGAACAGCAGTTTATTACTCTCTAAAGACAGA	ATGATGAGAA	1020					

Qy	1021	AGGCTGAATTTCTGTAATAAAGCAAAACAGCCTGCTTAGCAAGGAGCCACATAC	CAGAT	1080					
Db	1021	AGGCTGAATTTCTGTAATAAAGCAAAACAGCCTGCTTAGCAAGGAGCCACATAC	CAGAT	1080					
Qy	1081	GGGCTGGAAGTAAGAAACATGTAAATGATAGGCGGACTCCAGACACAGAA	AAAAAGGTAG	1140					
Db	1081	GGGCTGGAAGTAAGAAACATGTAAATGATAGGCGGACTCCAGACACAGAA	AAAAAGGTAG	1140					
Qy	1141	ATCTGAATGCTGATCCCTGTGTGAGAGAAAGAAATGGAATTAAGCAGAA	AACTGCATGCT	1200					
Db	1141	ATCTGAATGCTGATCCCTGTGTGAGAGAAAGAAATGGAATTAAGCAGAA	AACTGCATGCT	1200					
Qy	1201	CAGAGAACTCTAGAGATACCTGAGATGCTCTCTGGATAAACACTAAAT	TAGCAGATTGAGA	1260					
Db	1201	CAGAGAACTCTAGAGATACCTGAGATGCTCTCTGGATAAACACTAAAT	TAGCAGATTGAGA	1260					
Qy	1261	AAGTTAATGATGCTGTTTTCCAGAAAGTGAATGAACCTGTTAGGTTCT	GTGACTCACATGATG	1320					
Db	1261	AAGTTAATGATGCTGTTTTCCAGAAAGTGAATGAACCTGTTAGGTTCT	GTGACTCACATGATG	1320					
Qy	1321	GGGAGTCTGAATCAAAATGCCAAAGTAGCTGATGTATTGGACGTTCT	TAATAGAGTAGATG	1380					
Db	1321	GGGAGTCTGAATCAAAATGCCAAAGTAGCTGATGTATTGGACGTTCT	TAATAGAGTAGATG	1380					
Qy	1381	AATATTTCTGCTTCTCAGAGAAATAGACTTACTGGCCAGTGATCCT	CATGAGGCTTTAA	1440					
Db	1381	AATATTTCTGCTTCTCAGAGAAATAGACTTACTGGCCAGTGATCCT	CATGAGGCTTTAA	1440					
Qy	1441	TATGTAAAGTGAAAGAGTTTCACTCCAAATCAGTAGAGAGTAATAT	TATTAAGACAAAAATAT	1500					
Db	1441	TATGTAAAGTGAAAGAGTTTCACTCCAAATCAGTAGAGAGTAATAT	TATTAAGACAAAAATAT	1500					
Qy	1501	TTGGGAAAACTTATCGGAAGAGGCAAGCCTCCCAAATTAAGCATGT	TAACGAAATC	1560					
Db	1501	TTGGGAAAACTTATCGGAAGAGGCAAGCCTCCCAAATTAAGCATGT	TAACGAAATC	1560					
Qy	1561	TAATTTATGAGGACATTTGTTACTGAGCCACAGATATACAGAGCGT	CCCTCACAATA	1620					
Db	1561	TAATTTATGAGGACATTTGTTACTGAGCCACAGATATACAGAGCGT	CCCTCACAATA	1620					
Qy	1621	AATTTAAAGCGTAAAGGAGACCTACATCAGCGCTTCACTCTGAGGAT	TTTTATCAAGAAAG	1680					
Db	1621	AATTTAAAGCGTAAAGGAGACCTACATCAGCGCTTCACTCTGAGGAT	TTTTATCAAGAAAG	1680					
Qy	1681	CAGATTGGCAGTTCAAAAGACTCCTGAAATGATAATCAGGAACTAA	CAAAACGGAGC	1740					
Db	1681	CAGATTGGCAGTTCAAAAGACTCCTGAAATGATAATCAGGAACTAA	CAAAACGGAGC	1740					
Qy	1741	AGAATGCTCAAGTCAGTAATTTACTTAATAGTGGTCATGAGATAA	AAACAAAAGGTGATT	1800					
Db	1741	AGAATGCTCAAGTCAGTAATTTACTTAATAGTGGTCATGAGATAA	AAACAAAAGGTGATT	1800					
Qy	1801	CTATTCAAGATGAGAAAAATCCCTAAACCAATAGAACTACCTCGA	AAAAAGAAATCTGCTTTCA	1860					
Db	1801	CTATTCAAGATGAGAAAAATCCCTAAACCAATAGAACTACCTCGA	AAAAAGAAATCTGCTTTCA	1860					
Qy	1861	AAACGAAAGCTGAACTTATTAAGCAGAGTATAAGCAATATGGA	AACTCGAAATTAATATCC	1920					
Db	1861	AAACGAAAGCTGAACTTATTAAGCAGAGTATAAGCAATATGGA	AACTCGAAATTAATATCC	1920					
Qy	1921	ACAAATTTCAAAAGCACTTAAAGAAATAGGCTGAGGAGAAAGT	CTTCTACAGGCAATATTC	1980					
Db	1921	ACAAATTTCAAAAGCACTTAAAGAAATAGGCTGAGGAGAAAGT	CTTCTACAGGCAATATTC	1980					
Qy	1981	ATCGCTTTGAACCTAGTAGTCAAGTAGAAATCTAAGCCCACT	TAATTTGTAATTCGAAA	2040					
Db	1981	ATCGCTTTGAACCTAGTAGTCAAGTAGAAATCTAAGCCCACT	TAATTTGTAATTCGAAA	2040					
Qy	2041	TTGATAGTTGTTCTAGCAGTGAAAGAGATAAAGAAAAAAGTACA	CAAAATGCGAGTCA	2100					
Db	2041	TTGATAGTTGTTCTAGCAGTGAAAGAGATAAAGAAAAAAGTACA	CAAAATGCGAGTCA	2100					



QY 2101 GGCACAGCAAACTCACTCACTGAGGTAAGAACTGCAACTGGAGCCCAAGA 2160  
DB 2101 GGCACAGCAAACTCACTCACTGAGGTAAGAACTGCAACTGGAGCCCAAGA 2160  
QY 2161 GTAAACAGCCAAATGAACAGCAAGTAAGAAAGACATGATACCTTTCCAGAGCTGA 2220  
DB 2161 GTAAACAGCCAAATGAACAGCAAGTAAGAAAGACATGATACCTTTCCAGAGCTGA 2220  
QY 2221 AGTTAA CAAATGCACTGGTTCTTTTACTAAGTGTTCAAATACCAGTGAACCTTAAAGAA 2280  
DB 2221 AGTTAA CAAATGCACTGGTTCTTTTACTAAGTGTTCAAATACCAGTGAACCTTAAAGAA 2280  
QY 2281 TTGTCAATCTAGCCCTTCCAGAGCAAGAAAGAAAGACATGAAACAGCTTAAAGTGT 2340  
DB 2281 TTGTCAATCTAGCCCTTCCAGAGCAAGAAAGAAAGACATGAAACAGCTTAAAGTGT 2340  
QY 2341 CTAAATATGCTGAAGACCCCAAGATCTCACTGTTAAGTGAAGAAAGGTTTGCAAACTG 2400  
DB 2341 CTAAATATGCTGAAGACCCCAAGATCTCACTGTTAAGTGAAGAAAGGTTTGCAAACTG 2400  
QY 2401 AAAGATCTGTAGAGAGTAGCAGTATTTCACTGTGTACCTGTGATCTGATTTGGCACTCAGG 2460  
DB 2401 AAAGATCTGTAGAGAGTAGCAGTATTTCACTGTGTACCTGTGATCTGATTTGGCACTCAGG 2460  
QY 2461 AAAGTATCTGTTACTGGAAGTTAGCACTCTAGGGAAGGCAAAACAGAACCAAAATAAT 2520  
DB 2461 AAAGTATCTGTTACTGGAAGTTAGCACTCTAGGGAAGGCAAAACAGAACCAAAATAAT 2520  
QY 2521 GTGTGAGTCAGTGTGAGCATTGAAACCCCAAGGACTTAATTCATGGTTGTTCCAAAG 2580  
DB 2521 GTGTGAGTCAGTGTGAGCATTGAAACCCCAAGGACTTAATTCATGGTTGTTCCAAAG 2580  
QY 2581 ATAAATAGAAATGACACAGAGGCTTTAAAGTATCCATTTGGGACATGAAAGTTAACCAAGTC 2640  
DB 2581 ATAAATAGAAATGACACAGAGGCTTTAAAGTATCCATTTGGGACATGAAAGTTAACCAAGTC 2640  
QY 2641 GGGAAACCAAGCATAGAAATGGAAGAAAGTGAATGCTCAGTATTTGCGAAGTACAT 2700  
DB 2641 GGGAAACCAAGCATAGAAATGGAAGAAAGTGAATGCTCAGTATTTGCGAAGTACAT 2700  
QY 2701 TCAAGGTTTCAAGCGGCAGTCATTTGCTCTGTTTTCAATCCAGGAAATGCGAAGAGG 2760  
DB 2701 TCAAGGTTTCAAGCGGCAGTCATTTGCTCTGTTTTCAATCCAGGAAATGCGAAGAGG 2760  
QY 2761 AATGTGCAACATCTCTGCCCCACCTGCGTCTTAAAGAAACAAAGTCAAAAGTCACTT 2820  
DB 2761 AATGTGCAACATCTCTGCCCCACCTGCGTCTTAAAGAAACAAAGTCAAAAGTCACTT 2820  
QY 2821 TTGAATGTGAACAAAAGGAAGAAATCAAGGAAAGAAATGAGTCTTAATATCAAGCCTGTAC 2880  
DB 2821 TTGAATGTGAACAAAAGGAAGAAATCAAGGAAAGAAATGAGTCTTAATATCAAGCCTGTAC 2880  
QY 2881 AGACAGTTAATATCACTGCGAGGCTTCTGTTGTTGTCAGAAAGATGAAGCCAGTTGATA 2940  
DB 2881 AGACAGTTAATATCACTGCGAGGCTTCTGTTGTTGTCAGAAAGATGAAGCCAGTTGATA 2940  
QY 2941 ATGCGCAATGTAGTATCAAGGAGGCTCTAGGTTTGTCTATCATCTCAGTTCAAGGSCA 3000  
DB 2941 ATGCGCAATGTAGTATCAAGGAGGCTCTAGGTTTGTCTATCATCTCAGTTCAAGGSCA 3000  
QY 3001 ACGAAA CTGGACTCATTTACTCCAAATAAACATGGAATTTTACAAAACCCATATCGTATAC 3060  
DB 3001 ACGAAA CTGGACTCATTTACTCCAAATAAACATGGAATTTTACAAAACCCATATCGTATAC 3060  
QY 3061 CACCACCTTTTCCCACTCAAGTCAATTTGTTAAAACTAAATGTAAGAAAAATCTGCTAGAGG 3120  
DB 3061 CACCACCTTTTCCCACTCAAGTCAATTTGTTAAAACTAAATGTAAGAAAAATCTGCTAGAGG 3120  
QY 3121 AAAATTTTGAGAACATTCATGTCACCTGAAGGAAATGGGAAATGAGAACATTTCCNA 3180  
DB 3121 AAAATTTTGAGAACATTCATGTCACCTGAAGGAAATGGGAAATGAGAACATTTCCNA 3180  
QY 3181 GTACAGTGAGCAAAATTAGCCGTAATAACATTAGAGAAATGTTTTTAAAGGAGCCAGCT 3240

DB 3181 GTACAGTGAGCAAAATTAGCCGTAATAACATTAGAGAAATGTTTTTAAAGGAGCCAGCT 3240  
QY 3241 CAAGCAATATTAATGAAGTAGGTTCCAGTACTTAATGAAGTGGGCTCCAGTATTAAATGAAA 3300  
DB 3241 CAAGCAATATTAATGAAGTAGGTTCCAGTACTTAATGAAGTGGGCTCCAGTATTAAATGAAA 3300  
QY 3301 TAGGTTCCAGTGTAGTAAAAATCAACAGCAAACTAGGTAGAAAACAGAGGGCCAAAATTGA 3360  
DB 3301 TAGGTTCCAGTGTAGTAAAAATCAACAGCAAACTAGGTAGAAAACAGAGGGCCAAAATTGA 3360  
QY 3361 ATGCTATGCTTAGATTAGGGGTTTTGCAACTGAGGCTTATAAACAAGTCTTCTCGAA 3420  
DB 3361 ATGCTATGCTTAGATTAGGGGTTTTGCAACTGAGGCTTATAAACAAGTCTTCTCGAA 3420  
QY 3421 GTAATTTGAAGCATCTCGAAATAAAAAGCAAGAAATATGAAGTAGTTCAGACTGTTA 3480  
DB 3421 GTAATTTGAAGCATCTCGAAATAAAAAGCAAGAAATATGAAGTAGTTCAGACTGTTA 3480  
QY 3481 ATACAGATTTCTCTCCATATCTGATTTTCAAGATACTTAGAAACAGCCTATGGGAAGTAGTC 3540  
DB 3481 ATACAGATTTCTCTCCATATCTGATTTTCAAGATACTTAGAAACAGCCTATGGGAAGTAGTC 3540  
QY 3541 ATGCACTCTCAGGTTTGTCTGAGACACCTGATGACCTGTTAGATGATGGTGAATAAAGG 3600  
DB 3541 ATGCACTCTCAGGTTTGTCTGAGACACCTGATGACCTGTTAGATGATGGTGAATAAAGG 3600  
QY 3601 AAGATCTCTAGTTTGTCTGAAAAATGACATTAAGGAAAGTTCTGCTGTTTTTGTAGCAAAAGCG 3660  
DB 3601 AAGATCTCTAGTTTGTCTGAAAAATGACATTAAGGAAAGTTCTGCTGTTTTTGTAGCAAAAGCG 3660  
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DB 3661 TCCAGAGAGGAGAGCTTTAGCAGGAGTCTTAGCCCTTTCAACCCATACACATTTGCTCAGG 3720  
QY 3721 GTTACCGAAGAGGGGCCAAGAAATTAGAGTCTCAGAAAGAGAACTTATCTAGTGAGGATG 3780  
DB 3721 GTTACCGAAGAGGGGCCAAGAAATTAGAGTCTCAGAAAGAGAACTTATCTAGTGAGGATG 3780  
QY 3781 AAGAGCTTCCCTGCTTCCAAACACTGTTTATTTGGTAAAGTAAACAATATCTCTCAGT 3840  
DB 3781 AAGAGCTTCCCTGCTTCCAAACACTGTTTATTTGGTAAAGTAAACAATATCTCTCAGT 3840  
QY 3841 CTACTAGGCATAGCACCGTTGCTACCGAGTGTCTGCTTAAGAAACACAGAGAGAGAAATTTAT 3900  
DB 3841 CTACTAGGCATAGCACCGTTGCTACCGAGTGTCTGCTTAAGAAACACAGAGAGAGAAATTTAT 3900  
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DB 3901 TATCATTGAAGAAATAGCTTAAATGACTGCGATTAACAGGTAAATTTGGCAAGGCAATCTC 3960  
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DB 3961 AGGAACTACCTTAGTGAGGAAACAAATGTTCTGCTAGCTTCTTCTTCTCAGAGTGA 4020  
QY 4021 GTGAATTTGGAAGACTTCACTGCAAAATCAAAACACCCAGGATCCTTTCTTGAATGGTCTT 4080  
DB 4021 GTGAATTTGGAAGACTTCACTGCAAAATCAAAACACCCAGGATCCTTTCTTGAATGGTCTT 4080  
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QY 4261 ACTGCTCAGGCTATCTCTCAGAGTGAACATTTTAAACCACTCAGCAGAGGATACCATGC 4320

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Qy 4561 CAGATAGTTCTACAGTAAATAAAGAACCCAGAGTGGAAAGTCAATCCCTTCTAAAT 4620  
Db 4561 CAGATAGTTCTACAGTAAATAAAGAACCCAGAGTGGAAAGTCAATCCCTTCTAAAT 4620  
Qy 4621 GCCCATCATTAGATGATAGTGGTACATGACAGAGTTGCTCTGGAGTCTTCAGAAATAGAA 4680  
Db 4621 GCCCATCATTAGATGATAGTGGTACATGACAGAGTTGCTCTGGAGTCTTCAGAAATAGAA 4680  
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Db 4681 ACTACCCATCTCAAGAGAGCTCAATTAAGTTTGTATGTGGAGGACCAACAGCTGGAAG 4740  
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Qy 4801 CCCCTTACCTGGATCTGGATCAGCCTCTCTCTGATGACCCCTGAATCTGATCTCTCTG 4860  
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Db 4861 AAGACAGAGCCACAGAGTCTGCTGTGGCAACATACCATCTTCAACCTCTGCAATTGA 4920  
Qy 4921 AAGTTCCTCCAAATGAAAGTTGCAAGATCTGCCAGGCTCAGCTGTCTCATCTACTG 4980  
Db 4921 AAGTTCCTCCAAATGAAAGTTGCAAGATCTGCCAGGCTCAGCTGTCTCATCTACTG 4980  
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Db 4981 ATACTGCTGGTATATGCAATGGAAGAAAGTGTGAGCAGGAGAACCCAGAAATTGACAG 5040  
Qy 5041 CTTCAACAGAAAGGCTCAACAAAGAAATGTCATGTTGGTGTCTGGCTCAGCCCGAGAAG 5100  
Db 5041 CTTCAACAGAAAGGCTCAACAAAGAAATGTCATGTTGGTGTCTGGCTCAGCCCGAGAAG 5100  
Qy 5101 AATTTATGCTCGTGTACAAGTTTGCAGAAACACCAACATCATTAACTAATCTAATTA 5160  
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Qy 5161 CTGAAGAGACTACTCATGTTGTATGAAAACAGATGCTGATGTTGTGTGTAACGGACAC 5220  
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Qy 5221 TGAATAATTTTCTAGGAATTCGGGAGGAAATGGGTAGTATTCTCTGGGTGACCC 5280  
Db 5221 TGAATAATTTTCTAGGAATTCGGGAGGAAATGGGTAGTATTCTCTGGGTGACCC 5280  
Qy 5281 AGTCTATTAAAGAAAGAAAATGCTGAATGAGCATGATTTGAATCAGAGGAGATGCG 5340  
Db 5281 AGTCTATTAAAGAAAGAAAATGCTGAATGAGCATGATTTGAATCAGAGGAGATGCG 5340  
Qy 5341 TCAATGGAAGAAACCACAGGTTCCAAAGGACCAAGCAAGATCCAGGACAGAAATCT 5400  
Db 5341 TCAATGGAAGAAACCACAGGTTCCAAAGGACCAAGCAAGATCCAGGACAGAAATCT 5400

Qy 5401 TCAGGGGGCTAGAAATCTGTTGCTATGGGCCCTTACCAACATGCCACAGATCAACTGG 5460  
Db 5401 TCAGGGGGCTAGAAATCTGTTGCTATGGGCCCTTACCAACATGCCACAGATCAACTGG 5460  
Qy 5461 AATGGATGGTACAGCTGTGTGGTCTCTGTGTGGAAGGAGCTTTCATCTACCCCTTG 5520  
Db 5461 AATGGATGGTACAGCTGTGTGGTCTCTGTGTGGAAGGAGCTTTCATCTACCCCTTG 5520  
Qy 5521 GCACAGGTGCCACCCCAATTTGTTGTCAGCAGATGCTGTCAGAGGACATGGCT 5580  
Db 5521 GCACAGGTGCCACCCCAATTTGTTGTCAGCAGATGCTGTCAGAGGACATGGCT 5580  
Qy 5581 TCCATGCAATTTGGCAGATGTGAGGCACCTGTGTGGTGAACCCAGAGTGGTGTGGACA 5640  
Db 5581 TCCATGCAATTTGGCAGATGTGAGGCACCTGTGTGGTGAACCCAGAGTGGTGTGGACA 5640  
Qy 5641 GTGTAGCACTCTACCAAGTCCAGAGCTGGAACCTACCTGATATACCCAGATCCCCACA 5700  
Db 5641 GTGTAGCACTCTACCAAGTCCAGAGCTGGAACCTACCTGATATACCCAGATCCCCACA 5700  
Qy 5701 GCCACTACTGA 5711  
Db 5701 GCCACTACTGA 5711

RESULT 9  
AAV46454  
ID AAV46454 standard; cDNA; 5711 BP.  
XX AAV46454;  
AC AC  
XX XX  
DT 18-NOV-1998 (first entry)  
XX Human BRCA1 omil polymorphism #4 cDNA.  
DE BRCA1; omil; human; breast and ovarian cancer predisposing gene;  
XX polymorphism; susceptibility; anti-oncogene; tumour suppressor;  
KW chromosome 17q; ss.  
KW Homo sapiens.  
OS XX  
Key Location/Qualifiers  
FH 120..5711  
CDS FT  
FT /\*tag= a "BRCA1 omil protein"  
FT /product= b  
FT variation 3232  
FT /\*tag= b  
FT /note= "This polymorphic variation can be an A or G  
nucleotide"  
XX  
US5750400-A.  
PN  
XX  
XX 12-MAY-1998.  
PD  
XX  
XX 12-FEB-1997; 97US-0798691.  
PP  
XX  
XX 12-FEB-1996; 96US-0598591.  
PR  
XX 12-FEB-1997; 97US-0798691.  
PR  
XX  
XX (ONCO-) ONCORMED INC.  
PA  
XX  
XX Allen AC, Alvares CP, Critz BS, Murphy PD, Olson SJ;  
PI Schelter DB, Zeng B;  
PI  
XX WPI; 1998-296774/26.  
DR  
XX  
XX BRCA1 omi gene coding sequences - useful for distinguishing between  
PT polymorphisms and mutation(s) in the screening for disposition to  
PT breast or ovarian cancer  
XX  
PS Claim 2e; Page -; 54pp; English.  
XX

CC This sequence encodes a human BRCA1 (breast and ovarian cancer  
CC predisposing gene) om1 gene in which a polymorphic variation occurs at  
CC nucleotide 3232. This sequence and other polymorphic variations of this  
CC sequence are useful for the identification of an individual who may or  
CC may not have an increased susceptibility to breast or ovarian cancer.  
CC The sequences used identify gene changes which are due to polymorphisms,  
CC rather than cancer causing mutations. BRCA1 is an anti-oncogene (tumour  
CC suppressor) which is involved in genetic inheritance of cancers,  
CC especially breast and ovarian cancer. It is found at human chromosome  
CC 17q which is known to be linked to cancer susceptibility, especially  
CC breast cancer. Cells containing a mutation in this gene lose the  
CC wild-type function of BRCA1 and are more susceptible to cancers.  
CC NOTE: This sequence does not appear in the specification but has been  
CC created from the wild type BRCA1 om1 gene represented in AAV46448.  
XX  
SQ Sequence 5711 BP; 1953 A; 1099 C; 1276 G; 1382 T; 1 other;

Query Match 100.0%; Score 5710.6; DB 19; Length 5711;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 5710; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AGCTCGCTGAGACTTCCTGGACCCCGCACAGGCTGTGGGTTTCTCAGATAAAGTGGCC 60  
Db 1 AGCTCGCTGAGACTTCCTGGACCCCGCACAGGCTGTGGGTTTCTCAGATAAAGTGGCC 60

Qy 61 CCTGCGCTCAGGAGGCTTCACCTCTGCTCTGGGTAAAGTTTCAATGGAAACAGAAAGAAA 120  
Db 61 CCTGCGCTCAGGAGGCTTCACCTCTGCTCTGGGTAAAGTTTCAATGGAAACAGAAAGAAA 120

Qy 121 TGGATTTATCTGCTCTTCGGGTGAAGAGTACAAAATGCTAATTAAGTCTATGAGAAAA 180  
Db 121 TGGATTTATCTGCTCTTCGGGTGAAGAGTACAAAATGCTAATTAAGTCTATGAGAAAA 180

Qy 181 TCTTAGAGTGCCTATCTGCTGAGTTGTATCAAGGAGACCTGCTCCACAAAGTGTGACC 240  
Db 181 TCTTAGAGTGCCTATCTGCTGAGTTGTATCAAGGAGACCTGCTCCACAAAGTGTGACC 240

Qy 241 ACATATTTTGCATATTTGCAATCTGAACTTCTCAACAGAAAGGCGCTTTCACAGT 300  
Db 241 ACATATTTTGCATATTTGCAATCTGAACTTCTCAACAGAAAGGCGCTTTCACAGT 300

Qy 301 GTCTTTTATGATGATATACCAAAAGGAGCTTACAGAAAGTACGAGATTTAGTC 360  
Db 301 GTCTTTTATGATGATATACCAAAAGGAGCTTACAGAAAGTACGAGATTTAGTC 360

Qy 361 AACTTGTGAGAGCTATTGAAATCATTTTGTGCTTTTACGTTGACACAGGTTTGAGT 420  
Db 361 AACTTGTGAGAGCTATTGAAATCATTTTGTGCTTTTACGTTGACACAGGTTTGAGT 420

Qy 421 ATGCAACAGCTATAATTTTCAAAAAGGAGAAATTAATCTCTGCAACATCTAAAGATG 480  
Db 421 ATGCAACAGCTATAATTTTCAAAAAGGAGAAATTAATCTCTGCAACATCTAAAGATG 480

Qy 481 AAGTTTCTCATATCCAAAGTATGGCTACAGAAACCGTGCCAAAGACTTCTACAGAGTG 540  
Db 481 AAGTTTCTCATATCCAAAGTATGGCTACAGAAACCGTGCCAAAGACTTCTACAGAGTG 540

Qy 541 AACCAGAAATCTTCTTGTGAGAAACCACTCTCAGTGTCCAATCTCTAACCTTGGAA 600  
Db 541 AACCAGAAATCTTCTTGTGAGAAACCACTCTCAGTGTCCAATCTCTAACCTTGGAA 600

Qy 601 CTGTGAGAACTCTGAGGACAAAGCAGCGGATACAACTCTCAAAAGAGCTCTGTACATTG 660  
Db 601 CTGTGAGAACTCTGAGGACAAAGCAGCGGATACAACTCTCAAAAGAGCTCTGTACATTG 660

Qy 661 AATTGGGATCTGATTTCTCTGAGATACCGTTAATAAGCAACTTATTGTCAGTGTGGAG 720  
Db 661 AATTGGGATCTGATTTCTCTGAGATACCGTTAATAAGCAACTTATTGTCAGTGTGGAG 720

Qy 721 ATCAAGAAATTTGTTACAAATCTACCCCTCAAGGAAACAGGGATGAAATCAAGTTTGTG 780  
Db 721 ATCAAGAAATTTGTTACAAATCTACCCCTCAAGGAAACAGGGATGAAATCAAGTTTGTG 780

Qy 781 CAAAAAAGGCTGCTGTGTAATTTTCTGAGAGCGATGTAAACAAATACTGAACATCATCAAC 840  
Db 781 CAAAAAAGGCTGCTGTGTAATTTTCTGAGACGGATGTAAACAAATACTGAACATCATCAAC 840

Qy 841 CCAGTAAATATGATTTTGAACACACCTGAGAAAGCGTGCAGCTGAGAGGCGATCCAGAAAGT 900  
Db 841 CCAGTAAATATGATTTTGAACACACCTGAGAAAGCGTGCAGCTGAGAGGCGATCCAGAAAGT 900

Qy 901 ATCAGGGTAGTCTCTGTTTCAAACTTGCATGTGGAGCCATGTGGCACAATACTCATGCCA 960  
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Qy 961 GCTCATTTACAGATGAGAACAGACGATTTTATCTCCTCACTAAAGACAGAAATGATAGAAA 1020  
Db 961 GCTCATTTACAGATGAGAACAGACGATTTTATCTCCTCACTAAAGACAGAAATGATAGAAA 1020

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Qy 1081 GGGCTGGAAGTAAAGAAACATGTAATGATAGGCGGACTCCCAGCACAGAAAAAGGTAG 1140  
Db 1081 GGGCTGGAAGTAAAGAAACATGTAATGATAGGCGGACTCCCAGCACAGAAAAAGGTAG 1140

Qy 1141 ATCTGAATGCTGATCCCTCTGTGTGAGAGAAAGAAATGGAATAGCAGAAATCGCATGCT 1200  
Db 1141 ATCTGAATGCTGATCCCTCTGTGTGAGAGAAAGAAATGGAATAGCAGAAATCGCATGCT 1200

Qy 1201 CAGAGATCTCAGAGATACCTGAAAGATGTTCTTGGATAACACTAAATAGCAGCATTCAGA 1260  
Db 1201 CAGAGATCTCAGAGATACCTGAAAGATGTTCTTGGATAACACTAAATAGCAGCATTCAGA 1260

Qy 1261 AAGTTAATGATGTTGTTTCCAGAAAGTGAATGATGTTTCTGATGACTCAGATGATG 1320  
Db 1261 AAGTTAATGATGTTGTTTCCAGAAAGTGAATGATGTTTCTGATGACTCAGATGATG 1320

Qy 1321 GGGAGTCTGAATCAAAATGCCAAAGTAGCTGATGTTTGGACGTTCTAAATGAGGTAGATG 1380  
Db 1321 GGGAGTCTGAATCAAAATGCCAAAGTAGCTGATGTTTGGACGTTCTAAATGAGGTAGATG 1380

Qy 1381 AATATTTCTGTTTCTTCCAGAAATAGACTTACCTGCGCAGTGATCCTCATGAGGCTTTAA 1440  
Db 1381 AATATTTCTGTTTCTTCCAGAAATAGACTTACCTGCGCAGTGATCCTCATGAGGCTTTAA 1440

Qy 1441 TATGTAAAGTGAAGAGTTTCACTCCAAATCAGTAGAGAGTAAATATTGAAGACAAAAATAT 1500  
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Qy 1501 TTGGAAAACTTATCGGAAGAGGCAAGCCTCCCAACTTAAAGCCATGTAACTGAAAAATC 1560  
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Db 1681 CAGATTTGGCAGTTCAAAAGACTCTCTGAAATGATAAATCAGGGAACCTAACCAACGGAGC 1740

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Db 1741 AGAATGTCAGTGAATGAAATTAATTAATAGTGTGATGAGAAATTAATAAAGAGGTGATT 1800

Qy 1801 CTATTTCAAGATGAGAAAAATCCTTAACCCAAATAGAAATCACTCGAAAAAGAAATCTGCTTCA 1860  
Db 1801 CTATTTCAAGATGAGAAAAATCCTTAACCCAAATAGAAATCACTCGAAAAAGAAATCTGCTTCA 1860

Qy 1861 AAACGAAAGCTGAACTTATTAAGCAGCAGTATAAGCAATATGGAATCGAAATTAATATCC 1920



Qy	4081	CCAAA	CAAAATGAGGCATCAGTCTGAAAGCCAGGGAGTTGGTCTGAGTGA	CAAGGAATGG	4140				
Db									
Qy	4081	CCAAA	CAAAATGAGGCATCAGTCTGAAAGCCAGGGAGTTGGTCTGAGTGA	CAAGGAATGG	4140				
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Qy	4141	TTTCAG	ATGATGAAGAAGAGGACGGCTTGGAGAAATATCAAGAGACGAAGCA	4200					
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Qy	4141	TTTCAG	ATGATGAAGAAGAGGACGGCTTGGAGAAATATCAAGAGACGAAGCA	4200					
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Qy	4201	TGGATT	CAAACTTAGGTGAAGCAGCATCTGGGTGTGAGAGTGAAA	CAAGCGTCTCTGAAG	4260				
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Qy	4201	TGGATT	CAAACTTAGGTGAAGCAGCATCTGGGTGTGAGAGTGAAA	CAAGCGTCTCTGAAG	4260				
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Qy	4261	ACTGCT	CAGGGCTATCCTCTCAGAGTGACAATTTTAA	CCACTCAGCAGAGGGATACCATGC	4320				
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Qy	4261	ACTGCT	CAGGGCTATCCTCTCAGAGTGACAATTTTAA	CCACTCAGCAGAGGGATACCATGC	4320				
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Qy	4321	AACATA	ACCTGATTAAGCTCCAGCAGGAATGGCTGA	ACTAGAGCTGTGTAGAACAGC	4380				
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Qy	4501	GTGAAT	ACCCATTAAGCCAGAA	TCAGAAAGCCCTTCTGCTGACAGATT	TTGAGGTCGTCG	4560			
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Qy	4561	CAGATAG	CTCTAC	CAGTAAAAATAAGAAC	CCAGAGTGGAAGCTATCCCTTCTAAAT	4620			
Db									
Qy	4561	CAGATAG	CTCTAC	CAGTAAAAATAAGAAC	CCAGAGTGGAAGCTATCCCTTCTAAAT	4620			
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Qy	4741	AGTCTG	GGCCACAGATTTCAGGAAACATCTTACTTTCGCAAGCAGAGTCTAG	GGGAA	4800				
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Qy	4741	AGTCTG	GGCCACAGATTTCAGGAAACATCTTACTTTCGCAAGCAGAGTCTAG	GGGAA	4800				
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Qy	4801	CCCCTT	ACCTTGGAACTCTGGAA	TGAGCTCTCTGATGACCTTGAATCTGATCCTTCTG	4860				
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Qy	5041	CTTCAA	CAGAAAGGGTCAACAAA	AGAAATGTCCATGGTGGTGTCTGGGCTTGACCC	CAGAAG	5100			
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Db									

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Db	5161	CTGAAGAGACTCATCTGTTGTTATGAAGACAGATGCTGAGTTTGTGTGTAACGACAC	5220
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Db	5221	TGAAATATTTTCTAGGAATTGCCGGAGGAAATGGGTAGTTAGCTATTTCTGGGTGACCC	5280
Qy	5281	AGTCTATTAAAGAAAGAAAATGCTGAATGAGCATGATTTTGAAGTCAGAGGAGATGTGG	5340
Db	5281	AGTCTATTAAAGAAAGAAAATGCTGAATGAGCATGATTTTGAAGTCAGAGGAGATGTGG	5340
Qy	5341	TCAATGGAAGAAACCCAAAGGTCCTAAAGCGAGCAAGAGAAATCCAGGACAGAAAGATCT	5400
Db	5341	TCAATGGAAGAAACCCAAAGGTCCTAAAGCGAGCAAGAGAAATCCAGGACAGAAAGATCT	5400
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Db	5401	TCAGGGGGCTAGAAATCTGTGTCTATGGGCCCTTCCACCAATGCCACAGATCAACTGG	5460
Qy	5461	AATGGATGTGTACAGCTGTGTGGTGCTTCTGTGGTGAAGGAGCTTTTTCATCATTTCAACCTTG	5520
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Qy	5521	GCACAGGTGCCACCAATTTGTGGTTGTGTGAGCCAGATGCTTGGACAGAGCAATGGCT	5580
Db	5521	GCACAGGTGCCACCAATTTGTGGTTGTGTGAGCCAGATGCTTGGACAGAGCAATGGCT	5580
Qy	5581	TCCATGCAATTGGGCAGATGTGTGAGGCACCTGTGGTACCCGAGAGTGGGTCTTGGACA	5640
Db	5581	TCCATGCAATTGGGCAGATGTGTGAGGCACCTGTGGTACCCGAGAGTGGGTCTTGGACA	5640
Qy	5641	GTGTAGCACTCTACCAAGTGCAGAGCTGGACACCTACCTGATACCCAGATCCCCACA	5700
Db	5641	GTGTAGCACTCTACCAAGTGCAGAGCTGGACACCTACCTGATACCCAGATCCCCACA	5700
Qy	5701	GCCACTACTGA 5711	
Db	5701	GCCACTACTGA 5711	
RESULT 10			
AAV46455			
ID	AAV46455 standard; cDNA; 5711 BP.		
XX	AAV46455;		
AC	AAV46455;		
DT	18-NOV-1998 (first entry)		
XX	Human BRCA1 omil polymorphism #5 cDNA.		
DE	BRCA1; omil; human; breast and ovarian cancer predisposing gene;		
KW	polymorphism; susceptibility; anti-oncogene; tumour suppressor;		
KW	chromosome 17q; ss.		
XX	Homo sapiens.		
OS	Homo sapiens.		
XX	Key		
FT	Location/Qualifiers		
CDS	120..5711		
FT	/*tag= a		
FT	/*product= "BRCA1 omil protein"		
FT	3667		
FT	variation		
FT	/*tag= b		
FT	/*note= "This polymorphic variation can be an A or G		
FT	nucleotide"		
XX	US5750400-A.		
XX	12-MAY-1998.		
PD	12-FEB-1997;		
XX	97US-0798691.		
PF	12-FEB-1996;		
XX	96US-0598591.		

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PR 12-FEB-1997; 97US-0798691.
XX (ONCO-) ONCORMED INC.
XX
XX
XX Allen AC, Alvares CP, Critz BS, Murphy PD, Olson SJ;
XX Schelter DB, Zeng B;
XX
XX WPI; 1998-296774/26.
XX
XX BRCA1 omi gene coding sequences - useful for distinguishing between
XX polymorphisms and mutation(s) in the screening for disposition to
XX breast or ovarian cancer
XX
XX Claim 2e; Page -; 54pp; English.
XX
XX This sequence encodes a human BRCA1 (breast and ovarian cancer
XX predisposing gene) omi1 gene in which a polymorphic variation occurs at
XX nucleotide 3667. This sequence and other polymorphic variations of this
XX sequence are useful for the identification of an individual who may or
XX may not have an increased susceptibility to breast or ovarian cancer.
XX The sequences used identify gene changes which are due to polymorphisms,
XX rather than cancer causing mutations. BRCA1 is an anti-oncogene (tumour
XX suppressor) which is involved in genetic inheritance of cancers,
XX especially breast and ovarian cancer. It is found at human chromosome
XX 17q which is known to be linked to cancer susceptibility, especially
XX breast cancer. Cells containing a mutation in this gene lose the
XX wild-type function of BRCA1 and are more susceptible to cancers.
XX NOTE: This sequence does not appear in the specification but has been
XX created from the wild type BRCA1 omi1 gene represented in AAV4648.
XX
XX Sequence 5711 BP; 1953 A; 1099 C; 1276 G; 1382 T; 1 other;
XX
XX Query Match 100.0%; Score 5710.6; DB 19; Length 5711;
XX Best Local Similarity 100.0%; Pred. No. 0;
XX Matches 5710; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
XX
XX 1 AGCTCGCTGAGACTTCCTGGACCCCGCACAGGCTGTGGGTTTCTCAGATAACTGGGCC 60
XX
XX 1 AGCTCGCTGAGACTTCCTGGACCCCGCACAGGCTGTGGGTTTCTCAGATAACTGGGCC 60
XX
XX 61 CTGCGCTCAGGAGCCCTTCAACCTCTGCTCTGGGTTAAAGTTTCAATGGAAACAGAA 120
XX
XX 61 CTGCGCTCAGGAGCCCTTCAACCTCTGCTCTGGGTTAAAGTTTCAATGGAAACAGAA 120
XX
XX 121 TGGATTTATCTGCTCTCGGTTGAAGAAGTACAAATGTCATTAAGTCTATCGCAAAA 180
XX
XX 121 TGGATTTATCTGCTCTCGGTTGAAGAAGTACAAATGTCATTAAGTCTATCGCAAAA 180
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XX 181 TCTTAGAGTGTCCCATCTGCTGGAGTTGATCAAGGAACCTGTCTCCACAAAGTGTGACC 240
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XX 541 AACCCGAAATTCCTTCTTCAGGAAACCAAGTCTCAGTGTCCAACTCTCTAACCTTGGAA 600
XX

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Db 1621 AATTAAAGCGTAAAGAGGACCTACATCAGGCCCTTCATCTGAGGATTTTTATCAGAAAG 1680  
Qy 1681 CAGATTTGGCAGTTCAAAAGACTCCTGAAATGATAAATACGGGAACCTAACCAACGGAGC 1740  
Db 1681 CAGATTTGGCAGTTCAAAAGACTCCTGAAATGATAAATACGGGAACCTAACCAACGGAGC 1740  
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Qy 1861 AAACGAAAGCTGAACTTATTAAGCAGCAGTATAAGCAATATGGAACTCGAAATTAATATCC 1920  
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Db 1921 ACAATTCAAAAGCCTTAAAGAAATAGGCTGAGGAGGAAGTCTTCTACCGGCATATTC 1980  
Qy 1981 ATGGCTTTGAACCTAGTGTAGTAAATCTTAAGCCCACTTAATTTGACTGAATTTGCAAA 2040  
Db 1981 ATGGCTTTGAACCTAGTGTAGTAAATCTTAAGCCCACTTAATTTGACTGAATTTGCAAA 2040  
Qy 2041 TTGATAGTTGTTCTAGCAGTGAAGAGATAAAGAAAAAAGTACAACCAATGCCAGTCA 2100  
Db 2041 TTGATAGTTGTTCTAGCAGTGAAGAGATAAAGAAAAAAGTACAACCAATGCCAGTCA 2100  
Qy 2101 GGCA CAGCAGAAACCTCAACTCATGGAAGTAAAGAACTTGCAACTGGAGCCCAAGAGA 2160  
Db 2101 GGCA CAGCAGAAACCTCAACTCATGGAAGTAAAGAACTTGCAACTGGAGCCCAAGAGA 2160  
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Qy 3361 ATGCTATGCTTAGATTTAGGGGTTTTTGCAACTGAGGCTTATAAACAAGTCTTCTCGAA 3420  
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Qy 3421 GTAAATGTAGCACTCCGAAATAAAGCAAGAAATATGAAGTAGTCTCAGACTGTTA 3480  
Db 3421 GTAAATGTAGCACTCCGAAATAAAGCAAGAAATATGAAGTAGTCTCAGACTGTTA 3480  
Qy 3481 ATACAGATTTCTCTCCATATCTGATTTTCCAGATTAACCTTAGAACAGCCTATGGGAAGTAGTC 3540  
Db 3481 ATACAGATTTCTCTCCATATCTGATTTTCCAGATTAACCTTAGAACAGCCTATGGGAAGTAGTC 3540  
Qy 3541 ATGCATCTCAGGTTGTTCTGAGACACCTGATGACCTGTTAGATGATGGTGAATAAAGG 3600  
Db 3541 ATGCATCTCAGGTTGTTCTGAGACACCTGATGACCTGTTAGATGATGGTGAATAAAGG 3600  
Qy 3601 AAGTACTAGTTTGTGAAAAATGACATTAAGGAAAGTCTGCTGTTTTTATAGCAAAAGCG 3660  
Db 3601 AAGTACTAGTTTGTGAAAAATGACATTAAGGAAAGTCTGCTGTTTTTATAGCAAAAGCG 3660  
Qy 3661 TCCAGAGAGAGAGCTTTAGCAGGAGTCTTAGCCCTTTTACCCTATACATTTGGCTCAGG 3720  
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Db 3721 GTTACCGAAGAGGGGCAAGAAATTTAGAGTCTCAGAAAGAGAACTTATCTAGTGAGGATG 3780  
Qy 3781 AAGAGCTTCCCTGCTTCCAACTGTTTATTTGGTAAAGTAAACAATATACCTTCTCAGT 3840  
Db 3781 AAGAGCTTCCCTGCTTCCAACTGTTTATTTGGTAAAGTAAACAATATACCTTCTCAGT 3840

QY	3841	CTACTAGCATAGACCGTGTCTACCGAGTGTCTGTCTTAAGAAACACACAGAGAGAAATTTAT	3900
DB	3841	CTACTAGCATAGACCGTGTCTACCGAGTGTCTGTCTTAAGAAACACACAGAGAGAAATTTAT	3900
QY	3901	TATCATTTGAAGATAGCTTAAATGACCTGCGATACAGGTAAATATTGGCAAGGCATCTC	3960
DB	3901	TATCATTTGAAGATAGCTTAAATGACCTGCGATACAGGTAAATATTGGCAAGGCATCTC	3960
QY	3961	AGGAACATACACCTTAGTGAAGAAACAAATGTTCTGCTAGCTGTGTTTCTTCAAGTGCA	4020
DB	3961	AGGAACATACACCTTAGTGAAGAAACAAATGTTCTGCTAGCTGTGTTTCTTCAAGTGCA	4020
QY	4021	GTGAATTTGGAAGACTTGCACTGCAATAACAAACCCAGGATCCTTTCTTGATTTGTTCTT	4080
DB	4021	GTGAATTTGGAAGACTTGCACTGCAATAACAAACCCAGGATCCTTTCTTGATTTGTTCTT	4080
QY	4081	CCAAACAATAGGSCATCAGTCTGAAGCCAGGAGTTGGTCTGAGTGCAACAAGAAATGG	4140
DB	4081	CCAAACAATAGGSCATCAGTCTGAAGCCAGGAGTTGGTCTGAGTGCAACAAGAAATGG	4140
QY	4141	TTTCAGATGATGAAGAAAGAGGACGGCTTGGGAAGAAATATCAAGAAAGACCAAGCA	4200
DB	4141	TTTCAGATGATGAAGAAAGAGGACGGCTTGGGAAGAAATATCAAGAAAGACCAAGCA	4200
QY	4201	TGGAATCAAACTTAGTGAAGCAGCATCTGGGTGTGAGAGTGAAACAAAGCGTCTCTGAAG	4260
DB	4201	TGGAATCAAACTTAGTGAAGCAGCATCTGGGTGTGAGAGTGAAACAAAGCGTCTCTGAAG	4260
QY	4261	ACTGCTCAGGCTATCCTCTCAGAGTGACATTTTAAACCACTCAGCAGAGGATACCATGC	4320
DB	4261	ACTGCTCAGGCTATCCTCTCAGAGTGACATTTTAAACCACTCAGCAGAGGATACCATGC	4320
QY	4321	AACATACCTGATAAAGCTCCAGCAGGAATGGCTGAACCTAGAGCTGTGTAGAACAGC	4380
DB	4321	AACATACCTGATAAAGCTCCAGCAGGAATGGCTGAACCTAGAGCTGTGTAGAACAGC	4380
QY	4381	ATGGAGCCAGCCTTTCAACAGCTACCTTTCCATCAATAAGTGACTCTCTGCCCTTGAGG	4440
DB	4381	ATGGAGCCAGCCTTTCAACAGCTACCTTTCCATCAATAAGTGACTCTCTGCCCTTGAGG	4440
QY	4441	ACCTGGAAATCCAGAACCAAGCNCATCAGAAAAAGCAGTATTAACTTCAAGAAAGTA	4500
DB	4441	ACCTGGAAATCCAGAACCAAGCNCATCAGAAAAAGCAGTATTAACTTCAAGAAAGTA	4500
QY	4501	GTGAATACCTATAAGCCAGAAATCCAGAAAGCCTTTCTGCTGACAAAGTTTGGGTGCTG	4560
DB	4501	GTGAATACCTATAAGCCAGAAATCCAGAAAGCCTTTCTGCTGACAAAGTTTGGGTGCTG	4560
QY	4561	CAGATAGTTCTACCAAGTAAATAAAGAACCCAGAGTGGAAAGGTCAATCCCTTTCTAAAT	4620
DB	4561	CAGATAGTTCTACCAAGTAAATAAAGAACCCAGAGTGGAAAGGTCAATCCCTTTCTAAAT	4620
QY	4621	GCCCATCATTTAGATGATAGTGTTATCATGACAGTGTCTCTGGAGTCTTCAAGATAGAA	4680
DB	4621	GCCCATCATTTAGATGATAGTGTTATCATGACAGTGTCTCTGGAGTCTTCAAGATAGAA	4680
QY	4681	ACTACCCATCTCAAGAGGAGCTCATTAAGTGTGTGATGAGGAGGACACAGCTGGAAG	4740
DB	4681	ACTACCCATCTCAAGAGGAGCTCATTAAGTGTGTGATGAGGAGGACACAGCTGGAAG	4740
QY	4741	AGTCTGGGCCACACGATTTGACCGAAACATCTTACTTGGCCAAAGGATCTAGAGGGAA	4800
DB	4741	AGTCTGGGCCACACGATTTGACCGAAACATCTTACTTGGCCAAAGGATCTAGAGGGAA	4800
QY	4801	CCCTTACTTGGAATCTGGAATCAGCCTTCTCTGATGACCTGTAATCTGATCTCTCTG	4860
DB	4801	CCCTTACTTGGAATCTGGAATCAGCCTTCTCTGATGACCTGTAATCTGATCTCTCTG	4860
QY	4861	AAGACAGAGCCCGAGAGTCTGCTGCTGCGAACATACCATCTTCAACCTCTGCAATGA	4920
DB	4861	AAGACAGAGCCCGAGAGTCTGCTGCTGCGAACATACCATCTTCAACCTCTGCAATGA	4920
QY	4921	AAGTTCCTCCAAATTTGAAAGTTGCAGAAATCTGCCAGGCTCCAGCTGCTCATACTACTG	4980

DB	4921	AAGTTCCTCCAAATTTGAAAGTTGCAGAAATCTGCCAGGCTCCAGCTGCTCATACTACTG	4980
QY	4981	ATACTGCTGGTATATGCAATGGAAGAAAGTGTGAGCAGGAGGAGCCAGAAATTCAGAG	5040
DB	4981	ATACTGCTGGTATATGCAATGGAAGAAAGTGTGAGCAGGAGGAGCCAGAAATTCAGAG	5040
QY	5041	CTTCAACAGAAAGGGTCAACAAAGAAATGTCCATGGTGGTGTCTGGCTTCACCCAGAG	5100
DB	5041	CTTCAACAGAAAGGGTCAACAAAGAAATGTCCATGGTGGTGTCTGGCTTCACCCAGAG	5100
QY	5101	AATTTATGCTCGTGTACAAGTTTGCAGAAAAACCAACATCATCTTTAACTTAATTA	5160
DB	5101	AATTTATGCTCGTGTACAAGTTTGCAGAAAAACCAACATCATCTTTAACTTAATTA	5160
QY	5161	CTGAAGAGACTACTCATGTTGTTATGAAGAAACAGATGCTGAGTTTGTGTGAACGGACAC	5220
DB	5161	CTGAAGAGACTACTCATGTTGTTATGAAGAAACAGATGCTGAGTTTGTGTGAACGGACAC	5220
QY	5221	TGAAATATTTCTAGGAATTTGCGGAGGAGAAATGCGGTAGTTAGCTATTTCTGGGTGACCC	5280
DB	5221	TGAAATATTTCTAGGAATTTGCGGAGGAGAAATGCGGTAGTTAGCTATTTCTGGGTGACCC	5280
QY	5281	AGTCTATTAAAGAAAGAAATGCTGAATGAGCATGATTTTGAAGTCAGAGGAGATGTGG	5340
DB	5281	AGTCTATTAAAGAAAGAAATGCTGAATGAGCATGATTTTGAAGTCAGAGGAGATGTGG	5340
QY	5341	TCAATGGAAGAAACCAACCAAGTCCAAAGCGAGCAAGAAATCCAGGACAGAAAGATCT	5400
DB	5341	TCAATGGAAGAAACCAACCAAGTCCAAAGCGAGCAAGAAATCCAGGACAGAAAGATCT	5400
QY	5401	TCAGGGGCTAGAAATCTGTTGCTATGGGCCCTTACCAACATGCCACAGATCAACTGG	5460
DB	5401	TCAGGGGCTAGAAATCTGTTGCTATGGGCCCTTACCAACATGCCACAGATCAACTGG	5460
QY	5461	AATGGATGCTACAGCTGTGTGGTCTTCTGTGTGGAAGGAGCTTTTCATCTTCAACCTTG	5520
DB	5461	AATGGATGCTACAGCTGTGTGGTCTTCTGTGTGGAAGGAGCTTTTCATCTTCAACCTTG	5520
QY	5521	GCAAGGTGTCACCCCAATTTGGTTGTGAGCAGCAGATGCTTGCAGAGGACAAATGGCT	5580
DB	5521	GCAAGGTGTCACCCCAATTTGGTTGTGAGCAGCAGATGCTTGCAGAGGACAAATGGCT	5580
QY	5581	TCCATGCAATTTGGGCGAGATGTGAGGCACCTGTGTGTGACCCGAGAGTGGGTGGACA	5640
DB	5581	TCCATGCAATTTGGGCGAGATGTGAGGCACCTGTGTGTGACCCGAGAGTGGGTGGACA	5640
QY	5641	GTGTAGCACTTACCAAGTCCAGAGCTGAGACACCTACCTGTATACCCAGATCCCCACA	5700
DB	5641	GTGTAGCACTTACCAAGTCCAGAGCTGAGACACCTACCTGTATACCCAGATCCCCACA	5700
QY	5701	GCCACTACTGA 5711	
DB	5701	GCCACTACTGA 5711	

## RESULT 11

AAV46456  
ID AAV46456 standard; cDNA; 5711 BP.

XX AAV46456;

XX AC AC

XX DT 18-NOV-1998 (first entry)

XX Human BRCA1 omil polymorphism #6 cDNA.

XX BRCA1; omil; human; breast and ovarian cancer predisposing gene;

XX polymorphism; susceptibility; anti-oncogene; tumour suppressor;

XX chromosome 17q; ss.

XX Homo sapiens.

XX Key

XX Location/Qualifiers

FH

FT CDS 120..5711  
 FT /\*tag= a  
 FT /product= "BRCA1 omi protein"  
 FT 4427  
 FT variation  
 FT /\*tag= b  
 FT /note= "This polymorphic variation can be a T or C  
 FT nucleotide"  
 XX US5750400-A.  
 XX 12-MAY-1998. 97US-0798691.  
 XX 12-FEB-1997;  
 XX 12-FEB-1996;  
 XX 12-FEB-1997;  
 XX 96US-0598591.  
 XX 97US-0798691.  
 XX (ONCO-) ONCORMED INC.  
 XX Allen AC, Alvares CP, Critz BS, Murphy PD, Olson SJ;  
 XX Schelter DB, Zeng B;  
 XX WPI; 1998-296774/26.  
 XX BRCA1 omi gene coding sequences - useful for distinguishing between  
 XX polymorphisms and mutation(s) in the screening for disposition to  
 XX breast or ovarian cancer  
 XX Claim 2e; Page -; 54pp; English.  
 XX This sequence encodes a human BRCA1 (breast and ovarian cancer  
 XX predisposing gene) omi1 gene in which a polymorphic variation occurs at  
 XX nucleotide 4427. This sequence and other polymorphic variations of this  
 XX sequence are useful for the identification of an individual who may or  
 XX may not have an increased susceptibility to breast or ovarian cancer.  
 XX The sequences used identify gene changes which are due to polymorphisms,  
 XX rather than cancer causing mutations. BRCA1 is an anti-oncogene (tumour  
 XX suppressor) which is involved in genetic inheritance of cancers,  
 XX especially breast and ovarian cancer. It is found at human chromosome  
 XX 17q which is known to be linked to cancer susceptibility, especially  
 XX breast cancer. Cells containing a mutation in this gene lose the  
 XX wild-type function of BRCA1 and are more susceptible to cancers.  
 XX NOTE: This sequence does not appear in the specification but has been  
 XX created from the wild type BRCA1 omi1 gene represented in AAV46448.  
 XX Sequence 5711 BP; 1953 A; 1098 C; 1277 G; 1382 T; 1 other;  
 XX  
 Query Match 100.0%; Score 5710.6; DB 19; Length 5711;  
 Best Local Similarity 100.0%; Pred. No. 0;  
 Matches 5710; Conservative 1; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 AGCTCGCTGAGACTTCCTGGACCCCGCACAGGCTGTGGGTTTCTCAGATAACTGGGCC 60  
 DB |||||  
 QY 1 AGCTCGCTGAGACTTCCTGGACCCCGCACAGGCTGTGGGTTTCTCAGATAACTGGGCC 60  
 DB |||||  
 QY 61 CCTCGCTCAGAGGCGCTTCAACCTCTGCTCTGGGTAAAGTTCAATGGAAACAGAAAGAAA 120  
 DB |||||  
 QY 61 CCTCGCTCAGAGGCGCTTCAACCTCTGCTCTGGGTAAAGTTCAATGGAAACAGAAAGAAA 120  
 DB |||||  
 QY 121 TGGATTTATCTGCTCTTCGCGTTGAAGAGTACAAAATGTCATTAATGCTATGACAGAAA 180  
 DB |||||  
 QY 121 TGGATTTATCTGCTCTTCGCGTTGAAGAGTACAAAATGTCATTAATGCTATGACAGAAA 180  
 DB |||||  
 QY 181 TCTTAGAGTGCCCATCTGCTGAGTTGATCAAGGACCTGTCTCCACAAGTGTGACC 240  
 DB |||||  
 QY 181 TCTTAGAGTGCCCATCTGCTGAGTTGATCAAGGACCTGTCTCCACAAGTGTGACC 240  
 DB |||||  
 QY 241 ACATATTTGCAAAATTTTGATGCTGAAATCTTCAACAGAAAGAGGGCTTTCACAGT 300  
 DB |||||  
 QY 241 ACATATTTGCAAAATTTTGATGCTGAAATCTTCAACAGAAAGAGGGCTTTCACAGT 300  
 DB |||||  
 QY 301 GTCTTTTATGTAAGAATGATATAACCAAAAGGAGCCCTACAAAGAAAGTACAGATTTAGTC 360  
 DB |||||

Db 301 GTCTTTTATGTAAGAATGATATAACCAAAAGGAGCCCTACAAAGAAAGTACGAGATTTAGTC 360  
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 Db 361 AACTTGTGAGAGCTATTGAAAATCATTTGTGCTTTTGTAGCTTTGACACAGGTTGGAGT 420  
 QY 421 ATGCAACAGCTATAATTTTGCAGAAAAGGAAAATAACTCTCCTGGAACATCTAAAGATG 480  
 Db 421 ATGCAACAGCTATAATTTTGCAGAAAAGGAAAATAACTCTCCTGGAACATCTAAAGATG 480  
 QY 481 AAGTTTCTATCATCCAAAGTATGGCTACAGAAACCGTGCCAAAGAGCTTCTACAGAGTG 540  
 Db 481 AAGTTTCTATCATCCAAAGTATGGCTACAGAAACCGTGCCAAAGAGCTTCTACAGAGTG 540  
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 Db 541 AACCCGAAAATCCTTCTTGCAGGAAACCAAGTCTCAGTGCCAACTCTCTAACCTTGGAA 600  
 QY 601 CTGTGAGAACTCTGAGGACAAAAGCAGCGGATACAACTCTCAAAAGACGCTCTGTCTACATTG 660  
 Db 601 CTGTGAGAACTCTGAGGACAAAAGCAGCGGATACAACTCTCAAAAGACGCTCTGTCTACATTG 660  
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 Db 661 AATTGGGATCTGATTCTTCTGAAGATACCGTTAATAAGGCAACTTATTGCAAGTGTGGAG 720  
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 Db 721 ATCAAGAAATTTGTACAAATCACCCCTCAAGGAAACAGGAGTGAATCAGTTTGGATTCTG 780  
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Qy ||||| 3721 GTTACCAAGAGGGGCCAAGAAATAGAGTCTCAGAGAGAACTTATCTAGTGAGGATG 3780  
Db ||||| 3721 GTTACCAAGAGGGGCCAAGAAATAGAGTCTCAGAGAGAACTTATCTAGTGAGGATG 3780  
Qy ||||| 3781 AAGAGCTTCCCTGCTCCACACATGTTATTTGTTAAAGTAAACAATATACCTTCTCAGT 3840  
Db ||||| 3781 AAGAGCTTCCCTGCTCCACACATGTTATTTGTTAAAGTAAACAATATACCTTCTCAGT 3840  
Qy ||||| 3841 CTACTAGGCATAGCACCGTTGCTACCGAGTCTCTGTCTAAGAAACACAGAGAGAAATTTAT 3900  
Db ||||| 3841 CTACTAGGCATAGCACCGTTGCTACCGAGTCTCTGTCTAAGAAACACAGAGAGAAATTTAT 3900  
Qy ||||| 3901 TATCAATTGAAGATAGCTTAAATGACTGCAAGTAAACCAAGGTAAATTTGGCAAGCATCTC 3960  
Db ||||| 3901 TATCAATTGAAGATAGCTTAAATGACTGCAAGTAAACCAAGGTAAATTTGGCAAGCATCTC 3960  
Qy ||||| 3961 AGGAACATCACCCTTAGTGAGGAAACAAAATGTTCTGCTAGCTTGTCTTTCACAGTGCA 4020  
Db ||||| 3961 AGGAACATCACCCTTAGTGAGGAAACAAAATGTTCTGCTAGCTTGTCTTTCACAGTGCA 4020  
Qy ||||| 4021 GTGAATTTGGAGAGCTTGACTGCAAAATCAAAACACCCAGGATCCCTTTCTTGATTTGGTCTT 4080  
Db ||||| 4021 GTGAATTTGGAGAGCTTGACTGCAAAATCAAAACACCCAGGATCCCTTTCTTGATTTGGTCTT 4080  
Qy ||||| 4081 CCAAAACAAATGAGGCATCAGTCTGAAAGCCAGGAGTTGGTCTGAGTGACAAGGAAATGG 4140  
Db ||||| 4081 CCAAAACAAATGAGGCATCAGTCTGAAAGCCAGGAGTTGGTCTGAGTGACAAGGAAATGG 4140  
Qy ||||| 4141 TTTGAGATGATGAAGAGAGAAACGGGCTTTGGAAGAAAATAATCAAGAGAGCAAAAGCA 4200  
Db ||||| 4141 TTTGAGATGATGAAGAGAGAAACGGGCTTTGGAAGAAAATAATCAAGAGAGCAAAAGCA 4200  
Qy ||||| 4201 TGGATTCAAACTAGGTGAAGCAGCATCTGGGTGTGAGAGTGAACAGGCTCTCTGAAG 4260  
Db ||||| 4201 TGGATTCAAACTAGGTGAAGCAGCATCTGGGTGTGAGAGTGAACAGGCTCTCTGAAG 4260  
Qy ||||| 4261 ACTGCTCAGGCTATCTCTCAGAGTGACATTTTAAACCACTCAGCAGAGGAGTACCATGC 4320  
Db ||||| 4261 ACTGCTCAGGCTATCTCTCAGAGTGACATTTTAAACCACTCAGCAGAGGAGTACCATGC 4320  
Qy ||||| 4321 AACATAACCTGATAAAGCTCCAGCAGGAAATGGGCTGAACCTAGAGCTGTGTTAGAAACAGC 4380  
Db ||||| 4321 AACATAACCTGATAAAGCTCCAGCAGGAAATGGGCTGAACCTAGAGCTGTGTTAGAAACAGC 4380  
Qy ||||| 4381 ATGGAGCCAGCTTCTTAACAGCTACCTTCCATCATAGTGACTCTCTGCCCTTGAGG 4440  
Db ||||| 4381 ATGGAGCCAGCTTCTTAACAGCTACCTTCCATCATAGTGACTCTCTGCCCTTGAGG 4440  
Qy ||||| 4441 ACCTGCGAAATCCAGAACAAAGCAGCATCAGAAAAAGCAGTAACTTTACAGAAAAAGTA 4500  
Db ||||| 4441 ACCTGCGAAATCCAGAACAAAGCAGCATCAGAAAAAGCAGTAACTTTACAGAAAAAGTA 4500  
Qy ||||| 4501 GTGAATACCCCTTATAGCCAGAAATCCAGAAAGCCCTTTCTGCTGACAAGTTTGAGGTGCTG 4560  
Db ||||| 4501 GTGAATACCCCTTATAGCCAGAAATCCAGAAAGCCCTTTCTGCTGACAAGTTTGAGGTGCTG 4560  
Qy ||||| 4561 CAGATAGTTCTACAGGTAATAATAAGAAACAGAGGTGGAAGGTCTATCCCTTCTTAAT 4620  
Db ||||| 4561 CAGATAGTTCTACAGGTAATAATAAGAAACAGAGGTGGAAGGTCTATCCCTTCTTAAT 4620  
Qy ||||| 4621 GCCCATCATTAGATAGTGGTACATGACAGTTGCTCTGGGAGTCTTCAGATAGAA 4680  
Db ||||| 4621 GCCCATCATTAGATAGTGGTACATGACAGTTGCTCTGGGAGTCTTCAGATAGAA 4680  
Qy ||||| 4681 ACTACCCATCTCAAGAGAGCTCAATTAAGTTGTTGATGTGAGGAGCAACAGCTGGAAG 4740

Db ||||| 4681 ACTACCCATCTCAAGAGAGCTCAATTAAGTTGTTGATGTGAGGAGCAACAGCTGGAAG 4740  
Qy ||||| 4741 AGTCTGGGCCACACAGATTTGACGGAACAATCTTACTTTGCCAAGCAAGATCTAGAGGAA 4800  
Db ||||| 4741 AGTCTGGGCCACACAGATTTGACGGAACAATCTTACTTTGCCAAGCAAGATCTAGAGGAA 4800  
Qy ||||| 4801 CCCCTTACCTGGATCTGGAATCAGCCTCTCTCTGATGACCCCTGAATCTGATCTTCTG 4860  
Db ||||| 4801 CCCCTTACCTGGATCTGGAATCAGCCTCTCTCTGATGACCCCTGAATCTGATCTTCTG 4860  
Qy ||||| 4861 AAGCAGAGCCCCAGAGTCAAGTCTGTGTGGCAACATACCATTTCAACCTCTGCATTGA 4920  
Db ||||| 4861 AAGCAGAGCCCCAGAGTCAAGTCTGTGTGGCAACATACCATTTCAACCTCTGCATTGA 4920  
Qy ||||| 4921 AAGTTCCCAATTTGAAAGTTGCAAGTCTGCCAGGGTCCAGCTGTCTCATCTACTG 4980  
Db ||||| 4921 AAGTTCCCAATTTGAAAGTTGCAAGTCTGCCAGGGTCCAGCTGTCTCATCTACTG 4980  
Qy ||||| 4981 ATACTGCTGGGTATAATGCAATGGAAGAGTGTGAGCAGGAGAAAGCCAGAAATTGACAG 5040  
Db ||||| 4981 ATACTGCTGGGTATAATGCAATGGAAGAGTGTGAGCAGGAGAAAGCCAGAAATTGACAG 5040  
Qy ||||| 5041 CTTCAACAGAAAGGGTCAACAAAGAAATGTCATGTTGTTCTGTGGCTGACCCAGAAAG 5100  
Db ||||| 5041 CTTCAACAGAAAGGGTCAACAAAGAAATGTCATGTTGTTCTGTGGCTGACCCAGAAAG 5100  
Qy ||||| 5101 AATTTATGCTCGTGACAAAGTTTCCAGAAACACACATCACCTTTAACTTAATCTAATTA 5160  
Db ||||| 5101 AATTTATGCTCGTGACAAAGTTTCCAGAAACACACATCACCTTTAACTTAATCTAATTA 5160  
Qy ||||| 5161 CTGAAGAGACTACTCATGTTGTTATGAAAAACAGATGCTGAGTTTGTGTGAAACGAGCAC 5220  
Db ||||| 5161 CTGAAGAGACTACTCATGTTGTTATGAAAAACAGATGCTGAGTTTGTGTGAAACGAGCAC 5220  
Qy ||||| 5221 TGAATAATTTTCTAGGAATTTGCCGGAGGAAATCGGTAGTTAGCTATTCTTGGGTGACCC 5280  
Db ||||| 5221 TGAATAATTTTCTAGGAATTTGCCGGAGGAAATCGGTAGTTAGCTATTCTTGGGTGACCC 5280  
Qy ||||| 5281 AGTCTATTAAAGAAAGAAATGCTGAATGAGCATGATTTTGAAGTCAAGAGAGATGTGG 5340  
Db ||||| 5281 AGTCTATTAAAGAAAGAAATGCTGAATGAGCATGATTTTGAAGTCAAGAGAGATGTGG 5340  
Qy ||||| 5341 TCAATGGAAGAAACCAACCAAGGTCCAAAGCGAGCAAGAGAAATCCAGGACAGAAAGATCT 5400  
Db ||||| 5341 TCAATGGAAGAAACCAACCAAGGTCCAAAGCGAGCAAGAGAAATCCAGGACAGAAAGATCT 5400  
Qy ||||| 5401 TCAGGGGCTAGAAATCTGTTGCTATGGGCCCTTCAACCAATGCCACAGATCAACTGG 5460  
Db ||||| 5401 TCAGGGGCTAGAAATCTGTTGCTATGGGCCCTTCAACCAATGCCACAGATCAACTGG 5460  
Qy ||||| 5461 AATGATGGTACAGCTGTGTGCTCTGTGGTGAAGGAGCTTTTCATCTTACCCCTTG 5520  
Db ||||| 5461 AATGATGGTACAGCTGTGTGCTCTGTGGTGAAGGAGCTTTTCATCTTACCCCTTG 5520  
Qy ||||| 5521 GCA CAGGTGTCCACCCCAATTTGTGCTGTGACGAGCATGCTTGGACAGAGACAAATGGCT 5580  
Db ||||| 5521 GCA CAGGTGTCCACCCCAATTTGTGCTGTGACGAGCATGCTTGGACAGAGACAAATGGCT 5580  
Qy ||||| 5581 TCCATGCAATTTGGGAGAGATGTGTGAGGCACTGTGTGTAACCCGAGAGTGGGTGTTGGACA 5640  
Db ||||| 5581 TCCATGCAATTTGGGAGAGATGTGTGAGGCACTGTGTGTAACCCGAGAGTGGGTGTTGGACA 5640  
Qy ||||| 5641 GTGTAGCACTTACAGTGCAGGAGCTGGACACTTACCTGATCCCCCAGATCCCCCACA 5700  
Db ||||| 5641 GTGTAGCACTTACAGTGCAGGAGCTGGACACTTACCTGATCCCCCAGATCCCCCACA 5700  
Qy ||||| 5701 GCCACTACTGA 5711  
Db ||||| 5701 GCCACTACTGA 5711

ID AAV46457 standard; cDNA; 5711 BP.  
 AC AAV46457;  
 XX 18-NOV-1998 (first entry)  
 DT Human BRCA1 omil polymorphism #7 cDNA.  
 DE BRCA1; omil; human; breast and ovarian cancer predisposing gene;  
 XX polymorphism; susceptibility; anti-oncogene; tumour suppressor;  
 KW chromosome 17q; ss.  
 XX Homo sapiens.  
 OS  
 XX  
 XX Key Location/Qualifiers  
 PH 120..5711  
 FT /tag= a  
 FT /product= "BRCA1 omil protein"  
 FT 4956  
 FT variation  
 FT /tag= b  
 FT /note= "This polymorphic variation can be an A or G  
 nucleotide"  
 XX  
 PN US5750400-A.  
 XX 12-MAY-1998.  
 XX  
 PD 12-FEB-1997; 97US-0798691.  
 PF  
 PR 12-FEB-1996; 96US-0598591.  
 PR 12-FEB-1997; 97US-0798691.  
 XX  
 XX (ONCO-) ONCORMED INC.  
 XX  
 PI Allen AC, Alvares CP, Critz BS, Murphy PD, Olson SJ;  
 PI Schelter DB, Zeng B;  
 XX  
 DR WPI; 1998-296774/26.  
 XX  
 PT BRCA1 omi gene coding sequences - useful for distinguishing between  
 PT polymorphisms and mutation(s) in the screening for disposition to  
 PT breast or ovarian cancer  
 PS  
 PS Claim 2e; Page -; 54pp; English.  
 XX  
 CC This sequence encodes a human BRCA1 (breast and ovarian cancer  
 CC predisposing gene) omil gene in which a polymorphic variation occurs at  
 CC nucleotide 4956. This sequence and other polymorphic variations of this  
 CC sequence are useful for the identification of an individual who may or  
 CC may not have an increased susceptibility to breast or ovarian cancer.  
 CC The sequences used identify gene changes which are due to polymorphisms,  
 CC rather than cancer causing mutations. BRCA1 is an anti-oncogene (tumour  
 CC suppressor) which is involved in genetic inheritance of cancers,  
 CC especially breast and ovarian cancer. It is found at human chromosome  
 CC 17q which is known to be linked to cancer susceptibility, especially  
 CC breast cancer. Cells containing a mutation in this gene lose the  
 CC wild-type function of BRCA1 and are more susceptible to cancers.  
 CC NOTE: This sequence does not appear in the specification but has been  
 CC created from the wild type BRCA1 omil gene represented in AAV46448.  
 XX  
 SQ Sequence 5711 BP; 1953 A; 1099 C; 1276 G; 1382 T; 1 other;  
 Query Match 100.0%; Score 5710.6; DB 19; Length 5711;  
 Best Local Similarity 100.0%; Pred. No. 0;  
 Matches 5710; Conservative 1; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 AGCTCGCTGAGACTTCTCGACCCCGCACCAGGCTGTGGGTTTCTCAGATAACTGGGCC 60  
 DB 1 AGCTCGCTGAGACTTCTCGACCCCGCACCAGGCTGTGGGTTTCTCAGATAACTGGGCC 60  
 QY 61 CTTGCGCTCAGGAGGCTTCACTCTGTCTGTGGTAAAGTTTCATTGGAAACAGAAAGAAA 120  
 DB 61 CTTGCGCTCAGGAGGCTTCACTCTGTCTGTGGTAAAGTTTCATTGGAAACAGAAAGAAA 120



Qy	1201	CAGGAATCCTAGAGATACTGAAGATGTTCTTGGATAACTAAATAGCGATTCAGA	1260
Db	1201		
Qy	1261	AAGTTAATGAGTGTCTTTCAGAAAGTGAATGAATGTTAGGTTCTGATGACTCACATGATG	1320
Db	1261		
Qy	1321	GGGAGTCTGAATCAAAATGCCAAAGTAGCTGATGATTTGGAGCTTTAAATGAGGTAGATG	1380
Db	1321		
Qy	1381	AATATTCGTGTTCTTCAGAGAAAATAGACTTTACTTGGCCAGTGATCCTCATGAGCTTTAA	1440
Db	1381		
Qy	1441	TATGTAAAGTGAAGAGTTCACCTCCAAATCAGTAGAGAGTAATATTGAAGACAAAATAT	1500
Db	1441		
Qy	1501	TTGGGAAAACCTATCGGAAGAAGGCAAGCCTCCCAACTTAAGCCATGTAACTGAAAATC	1560
Db	1501		
Qy	1561	TAATTTATAGAGCATTTGTTACTGAGCCACAGATAATAAAGAGCGTCCCTCAAAATA	1620
Db	1561		
Qy	1621	AATTTAAAGCTTAAAGGAGACTACATCAGCGCTTCACTCCTGAGGATTTTATCAAGAAG	1680
Db	1621		
Qy	1681	CAGATTTGGCAGTTCAAAAGACTCCTGAAATGATAAATCAGGGAATTAACCAACGGAGC	1740
Db	1681		
Qy	1741	AGAAATGCTCAAGTGAATATTAATAATAGTGTCTATGAGAAATAAAACAAAAGTGAT	1800
Db	1741		
Qy	1801	CTATTCAGAAATGAGAAAATCCTAACCAATAGAAATCACTCGAAAAGAAATCTGCTTCA	1860
Db	1801		
Qy	1861	AAACGAAAGCTGAACCTTAAGCAGCAGTATAAGCAATATGCAATCTCGAAATTAATAATCC	1920
Db	1861		
Qy	1921	ACAAATTCAAAAGCACCTAAAAGAAATAGGCTGAGGAGGAAGTCTTTCTACCAAGGCATATTC	1980
Db	1921		
Qy	1981	ATGGCTTTGAATCTAGTAGTCAATGAAATCTAAGCCCACTTAATTTGATCTGAAATGCAAA	2040
Db	1981		
Qy	2041	TTGATAGTGTCTTAGCAGTGAAGATAAAGAAAAGTACAAACCAATGCCAGTCA	2100
Db	2041		
Qy	2101	GGCACAGAGAAAACCTACAACCTCATGGAAGGTAAAGAACCTTGCAACTGGAGCCCAAGAAGA	2160
Db	2101		
Qy	2161	GTAAACAGCCAAATGAAACAGCAAGTAAAAGACATGACAGTGATCTTTCCAGAGCTGA	2220
Db	2161		
Qy	2221	AGTTTAAACAAATGCACTGTTCTTTTCTAATAGTGTTCAAATCCAGTGAATCTTAAAGAAAT	2280
Db	2221		
Qy	2281	TTGTCAATCCTAGCCTTCCAAGAGAGAAAAGAGAGAACTAGAAAACAGTTAAAGTGT	2340
Db	2281		

Db	2281	TTGTCAATCCTAGCCTTCCAAGAGAGAAAAGAGAGAACTAGAAAACAGTTTAAAGTGT	2340
Qy	2341	CTAATAATGCTGAAGACCCCAAGATCTCATGTTAAAGTGGAGAAAGGTTTGGCAAACTG	2400
Db	2341		
Qy	2401	AAAGATCTGTAGAGAGTAGCAGTATTTCACTGGTACCTGGTACTGATTTATGGCACTCAGG	2460
Db	2401		
Qy	2461	AAAGTATCTCGTTACTGGAAAGTTAGCACTCTAGGGAAGGCAAAACAGAACCAATAAAT	2520
Db	2461		
Qy	2521	GTGTGAGTCAAGTGTGAGCAATTTGAAAACCCCAAGGACCTAAATTCATGGTTGTTCCAAAG	2580
Db	2521		
Qy	2581	ATAATAGAAATGACACAGAAAGGCTTTAAAGTATCCATTTGGGACATGAAGTTAACCAAGTC	2640
Db	2581		
Qy	2641	GGGAAACAAGCATAGAAAATGGAGAAAAGTGAACCTTGAATCTCAGTATTTGAGAAATACAT	2700
Db	2641		
Qy	2701	TCAGAGTTTCAAGGCGCAGTCATTGCTCTGTTTCAAAATCCAGGAAATGCAGAAAGG	2760
Db	2701		
Qy	2761	AATGTGCAACATTTCTGCCCCACTCTGGGCTCTTTAAAGAAAACAAAGTCCAAAAGTCATT	2820
Db	2761		
Qy	2821	TTGAATGTGAACAAAAGGAGAAAATCAAGGAAAGATGAGTCTTAATATCAAGCCTGTAC	2880
Db	2821		
Qy	2881	AGACAGTTTAATATACACTGCGGCTTTCTGTTGTTGTCAGAAAAGATGAAGCCAGTTGATA	2940
Db	2881		
Qy	2941	ATGCCAAATGTAGTATCAAAAGGAGGCTCTAGGTTTGTCTATCATCTCAGTTCCAGAGCA	3000
Db	2941		
Qy	3001	ACGAAACTGGAATCATTTCTCCAAATAAATGAGTCTTTTACAAAACCCATATCGTATAC	3060
Db	3001		
Qy	3061	CACCACCTTTTCCCATCAAGTCAATTTGTTAAACCTAAATGTAAGAAAATCTGCTAGAGG	3120
Db	3061		
Qy	3121	AAAACTTTGAGGAAACATTTCAATGTCACTGAAAAGGAAATGGGAAATGAGAACTTCCAA	3180
Db	3121		
Qy	3181	GTAAGTGAAGCAATTTAGCGGTAAATAATATTAGAGAAAATGTTTTTAAAGGAGCAGCT	3240
Db	3181		
Qy	3241	CAAGCAATTAATGAAGTAGGTTCCAGTACTAATGAGTGGCTCCAGTATTAAATGAAA	3300
Db	3241		
Qy	3301	TAGTTCCAGTGAAGAAAACATTTCAAGCAGAACTTAGGTAGAAAACAGAGGGCCAAATTTGA	3360
Db	3301		
Qy	3361	ATGCTATGCTTAGATTAGGGGTTTTGCAACTGAGGCTTATTAACAAAGTCTTCTCTGAAA	3420
Db	3361		



QY 5581 TCCATGCAATTGGGCGAGATGTGTAGGCACTGTGTGACCCGAGAGTGGGTGTGGACA 5640  
 Db |||||  
 QY 5581 TCCATGCAATTGGGCGAGATGTGTAGGCACTGTGTGACCCGAGAGTGGGTGTGGACA 5640  
 Db |||||  
 QY 5641 GTGTAGCACTCTACCAAGTCCAGGAGCTGGACACCTACCTGATACCCGAGATCCCCCACA 5700  
 Db |||||  
 QY 5701 GCCACTACTGA 5711  
 Db |||||  
 QY 5701 GCCACTACTGA 5711  
 Db |||||

RESULT 13  
 AAV46450  
 ID AAV46450 standard; cDNA; 5711 BP.  
 XX  
 AC AAV46450;  
 XX  
 DT 18-NOV-1998 (first entry)  
 DE Human BRCA1 omi3 cDNA.  
 XX  
 KW BRCA1; omi3; human; breast and ovarian cancer predisposing gene;  
 KW polymorphism; susceptibility; anti-oncogene; tumour suppressor;  
 KW chromosome 17q; ss.  
 XX  
 OS Homo sapiens.  
 XX  
 FH Key Location/Qualifiers  
 FT CDS 120..5711  
 FT /\*tag= a  
 FT /product= "BRCA1 omi3 protein"  
 XX

US5750400-A.  
 XX  
 PD 12-MAY-1998.  
 XX  
 PF 12-FEB-1997; 97US-0798691.  
 XX  
 PR 12-FEB-1996; 96US-0598591.  
 PR 12-FEB-1997; 97US-0798691.  
 XX  
 PA (ONCO-) ONCORMED INC.  
 XX  
 PI Allen AC, Alvares CP, Critz BS, Murphy PD, Olson SJ;  
 PI Schelter DB, Zeng B;  
 XX  
 DR WPI; 1998-296774/26.  
 DR P-ESDB; AAW76100.  
 XX  
 XX BRCA1 omi gene coding sequences - useful for distinguishing between  
 PT polymorphisms and mutation(s) in the screening for disposition to  
 PT breast or ovarian cancer  
 XX  
 PS Claim 2e; Column 55-62; 54pp; English.  
 XX  
 CC This sequence encodes the human BRCA1 (breast and ovarian cancer  
 CC predisposing gene) omi3 gene. This sequence and polymorphic variations of  
 CC this sequence are useful for the identification of an individual who may  
 CC or may not have an increased susceptibility to breast or ovarian cancer.  
 CC The sequences used identify gene changes which are due to polymorphisms,  
 CC rather than cancer causing mutations. BRCA1 is an anti-oncogene (tumour  
 CC suppressor) which is involved in genetic inheritance of cancers,  
 CC especially breast and ovarian cancer. It is found at human chromosome 17q  
 CC which is known to be linked to cancer susceptibility, especially breast  
 CC cancer. Cells containing a mutation in this gene lose the wild-type  
 CC function of BRCA1 and are more susceptible to cancers.  
 XX  
 SQ Sequence 5711 BP; 1953 A; 1098 C; 1277 G; 1383 T; 0 other;

Query Match 100.0%; Score 5709.4; DB 19; Length 5711;  
 Best Local Similarity 100.0%; Pred. No. 0;

Matches 5710; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
 QY 1 AGCTCGCTGAGACTTCCTGGACCCCGACACAGGCTGTGGGGTCTTCTCAGATAAAGTGGGCC 60  
 Db |||||  
 QY 1 AGCTCGCTGAGACTTCCTGGACCCCGACACAGGCTGTGGGGTCTTCTCAGATAAAGTGGGCC 60  
 Db |||||  
 QY 61 CCTCGCTCAGGAGGCGCTTCACTCTGCTCTGGGTAAAGTTTCATTTGGAACAGAAAGAAA 120  
 Db |||||  
 QY 61 CCTCGCTCAGGAGGCGCTTCACTCTGCTCTGGGTAAAGTTTCATTTGGAACAGAAAGAAA 120  
 Db |||||  
 QY 121 TGGATTTATCTGCTCTTGGGTTGAAGAAGTACAAAATGTCAATTAATCTATGCAAGAAA 180  
 Db |||||  
 QY 121 TGGATTTATCTGCTCTTGGGTTGAAGAAGTACAAAATGTCAATTAATCTATGCAAGAAA 180  
 Db |||||  
 QY 181 TCTTAGAGTGTCCCATCTGTCTGGAGTTGATCAAGGAACCTGTCTCCACAAAGTGTGACC 240  
 Db |||||  
 QY 181 TCTTAGAGTGTCCCATCTGTCTGGAGTTGATCAAGGAACCTGTCTCCACAAAGTGTGACC 240  
 Db |||||  
 QY 241 ACATATTTTGC AAAATTTTGCATGTCTGAAACCTTCTCAAC CAGAAAGGGCTTTCACAGT 300  
 Db |||||  
 QY 241 ACATATTTTGC AAAATTTTGCATGTCTGAAACCTTCTCAAC CAGAAAGGGCTTTCACAGT 300  
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 QY 301 GTCTCTTATGTAAAGATGATATAACCAAGAGGAGCTTACAGAAAGTACAGAGATTTAGTC 360  
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 QY 301 GTCTCTTATGTAAAGATGATATAACCAAGAGGAGCTTACAGAAAGTACAGAGATTTAGTC 360  
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 QY 361 AACTTGTGAGAGCTATTGAAAATCATTTGTGCTTTTTCAGCTTGTGACACAGGTTTGGAGT 420  
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 QY 361 AACTTGTGAGAGCTATTGAAAATCATTTGTGCTTTTTCAGCTTGTGACACAGGTTTGGAGT 420  
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 QY 421 ATGCAAAACAGCTATAAATTTTGC AAAAAGGAAAATAAATCTCTCTCTGAAACATCTAAAGATG 480  
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 QY 421 ATGCAAAACAGCTATAAATTTTGC AAAAAGGAAAATAAATCTCTCTCTGAAACATCTAAAGATG 480  
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 QY 481 AAGTTTCTATCATCCAAAGTATGCGCTACAGAAACCGTCCAAAAGACTTCTACAGAGTG 540  
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 QY 481 AAGTTTCTATCATCCAAAGTATGCGCTACAGAAACCGTCCAAAAGACTTCTACAGAGTG 540  
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 QY 541 AACCAGAAATCCCTTCTTGCAGGAAACCACTCTCAGTGTCCAACTCTCTAACCTTGGAA 600  
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 QY 541 AACCAGAAATCCCTTCTTGCAGGAAACCACTCTCAGTGTCCAACTCTCTAACCTTGGAA 600  
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 QY 601 CTGTGAGAACTCTGAGGACAAAAGCAGCGGATACAACTCTCAAAAGACGCTCTCTACATTTG 660  
 Db |||||  
 QY 601 CTGTGAGAACTCTGAGGACAAAAGCAGCGGATACAACTCTCAAAAGACGCTCTCTACATTTG 660  
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 QY 661 AATTGGGATCTGATTTCTTGAAGATACCGTTAAAGGGCAACTTATTGCGAGTGTGGAG 720  
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 QY 661 AATTGGGATCTGATTTCTTGAAGATACCGTTAAAGGGCAACTTATTGCGAGTGTGGAG 720  
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 QY 721 ATCAAGAAATTTGTACAAATCACCCCTCAAGGAACCGGATGAAATCAGTTTGGATTCTG 780  
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 QY 721 ATCAAGAAATTTGTACAAATCACCCCTCAAGGAACCGGATGAAATCAGTTTGGATTCTG 780  
 Db |||||  
 QY 781 CAAAAAAGGCTGTGTGAAATTTTCTGAGCGGATGTAACAAATCTGAAACATCATCAAC 840  
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 QY 781 CAAAAAAGGCTGTGTGAAATTTTCTGAGCGGATGTAACAAATCTGAAACATCATCAAC 840  
 Db |||||  
 QY 841 CCAGTAATATGATTTGAAACCACTGAGAAAGCGTGCAGCTGAGAGGATCCAGAAAGT 900  
 Db |||||  
 QY 841 CCAGTAATATGATTTGAAACCACTGAGAAAGCGTGCAGCTGAGAGGATCCAGAAAGT 900  
 Db |||||  
 QY 901 ATCAGGCTAGTCTGTTTCAAACTTGCATGTGGAGCCATGTGGCACAATACTCATGCCA 960  
 Db |||||  
 QY 901 ATCAGGCTAGTCTGTTTCAAACTTGCATGTGGAGCCATGTGGCACAATACTCATGCCA 960  
 Db |||||  
 QY 961 GCTCATTTACAGCATGAGAACAGAGTATTATTACTCTACTTAAAGACAGAGTGAATGTAGAAA 1020  
 Db |||||  
 QY 961 GCTCATTTACAGCATGAGAACAGAGTATTATTACTCTACTTAAAGACAGAGTGAATGTAGAAA 1020  
 Db |||||  
 QY 1021 AGGCTGAATTTCTGTAATTAAGCAAAACAGCTGTGCTTAGCAAGGAGGCAACATACAGAT 1080  
 Db |||||  
 QY 1021 AGGCTGAATTTCTGTAATTAAGCAAAACAGCTGTGCTTAGCAAGGAGGCAACATACAGAT 1080  
 Db |||||

Qy	1081	GGGCTGGAAGTAAGGAAACATGTATGATAGCGGACTCCAGACAGAAAAAAGGTAG	1140
Db	1081	GGGCTGGAAGTAAGGAAACATGTATGATAGCGGACTCCAGACAGAAAAAAGGTAG	1140
Qy	1141	ATCTGAATGCTGATCCCTGTGTGAGAGAAAGAAATGGAATPAAGCAGAAACTGCCATGCT	1200
Db	1141	ATCTGAATGCTGATCCCTGTGTGAGAGAAAGAAATGGAATPAAGCAGAAACTGCCATGCT	1200
Qy	1201	CAGAGAACTCTAGAGATACGAAGATGTTCTTGGATAACAATAAGTAGCAGCATTCAGA	1260
Db	1201	CAGAGAACTCTAGAGATACGAAGATGTTCTTGGATAACAATAAGTAGCAGCATTCAGA	1260
Qy	1261	AAGTTAATGATGCTGTTTTCCAGAGAGTGAATCACTGTTAGGTTCTGTGACCTCAATGATG	1320
Db	1261	AAGTTAATGATGCTGTTTTCCAGAGAGTGAATCACTGTTAGGTTCTGTGACCTCAATGATG	1320
Qy	1321	GGGAGTCTGAATCAAAATGCCAAAGTAGCTGATGTAATTGGACGTTCTAAATGAGGTAGATG	1380
Db	1321	GGGAGTCTGAATCAAAATGCCAAAGTAGCTGATGTAATTGGACGTTCTAAATGAGGTAGATG	1380
Qy	1381	AATATTCTGGTTCTTCAGAGAAATAGACTTACTGGCCAGTGAATCCTCATGAGGCTTTAA	1440
Db	1381	AATATTCTGGTTCTTCAGAGAAATAGACTTACTGGCCAGTGAATCCTCATGAGGCTTTAA	1440
Qy	1441	TATCTAAAGTGAAGAGAGTTCACTCCAAATCAGTAGAGAGTAATATTGAAGACAAAATAT	1500
Db	1441	TATCTAAAGTGAAGAGAGTTCACTCCAAATCAGTAGAGAGTAATATTGAAGACAAAATAT	1500
Qy	1501	TTGGGAAACCTATCGGAAGAGCAAGCCCTCCCACTTAAAGCCATGTAACTGAAATC	1560
Db	1501	TTGGGAAACCTATCGGAAGAGCAAGCCCTCCCACTTAAAGCCATGTAACTGAAATC	1560
Qy	1561	TAATTAAGGAGCATTTGTACTCAGCCACAGATAATACAGAGCGTCCCTCAAAATA	1620
Db	1561	TAATTAAGGAGCATTTGTACTCAGCCACAGATAATACAGAGCGTCCCTCAAAATA	1620
Qy	1621	AATTAAGCGTAAAGGAGACCTACATCAGCGCTTCACTCAGGATTTTATCAAGAAAG	1680
Db	1621	AATTAAGCGTAAAGGAGACCTACATCAGCGCTTCACTCAGGATTTTATCAAGAAAG	1680
Qy	1681	CAGATTTGGGAGTTCAAAAGACTCCTGAAATGATAATACAGGAACTTAACAAACGGAGC	1740
Db	1681	CAGATTTGGGAGTTCAAAAGACTCCTGAAATGATAATACAGGAACTTAACAAACGGAGC	1740
Qy	1741	AGATGCTCAAGTCATGAATATTACTAATAGTGTGATGAGATAAAGAAAGGTGATT	1800
Db	1741	AGATGCTCAAGTCATGAATATTACTAATAGTGTGATGAGATAAAGAAAGGTGATT	1800
Qy	1801	CTATTCAAGATGAGAAAAATCCTAACCAATAGAAATCACTCGAAAAAGAAATCTGCTTTCA	1860
Db	1801	CTATTCAAGATGAGAAAAATCCTAACCAATAGAAATCACTCGAAAAAGAAATCTGCTTTCA	1860
Qy	1861	AAAGAAAGCTGAACCTATAGCAGCAGTATAGCAATATGGAATCGAATTAATATCC	1920
Db	1861	AAAGAAAGCTGAACCTATAGCAGCAGTATAGCAATATGGAATCGAATTAATATCC	1920
Qy	1921	ACAAATCAAGGACCTTAAAGAAATAGGCTGAGGAGAACTTCTTACAGGCAATATTC	1980
Db	1921	ACAAATCAAGGACCTTAAAGAAATAGGCTGAGGAGAACTTCTTACAGGCAATATTC	1980
Qy	1981	ATGGCTTTGAACCTAGTAGTCACTAAGCAATCTAAGCCACCTAATTGTACTGAATTCGAAA	2040
Db	1981	ATGGCTTTGAACCTAGTAGTCACTAAGCAATCTAAGCCACCTAATTGTACTGAATTCGAAA	2040
Qy	2041	TTGATGTTGTTTACAGTGAAGAGATAAGAAAAAAGTACAAACAAATGCCAGTCA	2100
Db	2041	TTGATGTTGTTTACAGTGAAGAGATAAGAAAAAAGTACAAACAAATGCCAGTCA	2100
Qy	2101	GGCAGCAGAAACCTACAACTATGAGGTGAAGAACTGCAACTGGAGCCAGAGAA	2160
Db	2101	GGCAGCAGAAACCTACAACTATGAGGTGAAGAACTGCAACTGGAGCCAGAGAA	2160

Qy	2161	GTAACAAAGCCAAATGAACAGACAGTAAGTAAAGACATGACAGTGATCTTTCCAGAGCTGA	2220
Db	2161	GTAACAAAGCCAAATGAACAGACAGTAAGTAAAGACATGACAGTGATCTTTCCAGAGCTGA	2220
Qy	2221	AGTTAAACAAATGACCTGGTTCTTTTACTAAGTGTTCAAATPAACAGTGAACCTTAAAGAAT	2280
Db	2221	AGTTAAACAAATGACCTGGTTCTTTTACTAAGTGTTCAAATPAACAGTGAACCTTAAAGAAT	2280
Qy	2281	TTGTCATATCTAGCTTCCAGAGAGAGAAAAAGAGAGAACTAGAAACAGTGTAAAGTGT	2340
Db	2281	TTGTCATATCTAGCTTCCAGAGAGAGAAAAAGAGAGAACTAGAAACAGTGTAAAGTGT	2340
Qy	2341	CTAATAATGCTGAAGACCCCAAGATCTCATGTTAAGTGAAGAAAGGTTTTCGAAACTG	2400
Db	2341	CTAATAATGCTGAAGACCCCAAGATCTCATGTTAAGTGAAGAAAGGTTTTCGAAACTG	2400
Qy	2401	AAAGATCTGTAGAGAGTACCTGTTTCACTGGTACTGGTACTGATTTATGGCACTCAGG	2460
Db	2401	AAAGATCTGTAGAGAGTACCTGTTTCACTGGTACTGGTACTGATTTATGGCACTCAGG	2460
Qy	2461	AAAGTATCTCGTTACTGGAAGTTAGCACTCTAGGGAAGGCAAAAACAGAACCAATTAAT	2520
Db	2461	AAAGTATCTCGTTACTGGAAGTTAGCACTCTAGGGAAGGCAAAAACAGAACCAATTAAT	2520
Qy	2521	GTGTGAGTCAAGTGTGACAGCATTTGAAAAACCCCAAGGACTTAATTCATGGTGTTCGAAAG	2580
Db	2521	GTGTGAGTCAAGTGTGACAGCATTTGAAAAACCCCAAGGACTTAATTCATGGTGTTCGAAAG	2580
Qy	2581	ATAATAGAAATGACACAGAAAGGCTTTTAAAGTATCCATTTGGGACATGAAGTTAAACACAGTC	2640
Db	2581	ATAATAGAAATGACACAGAAAGGCTTTTAAAGTATCCATTTGGGACATGAAGTTAAACACAGTC	2640
Qy	2641	GSGAAACAAAGCATAGAAATGGAAGAGTGAACCTTGATGCTCAGTATTTCCGAGNATACAT	2700
Db	2641	GSGAAACAAAGCATAGAAATGGAAGAGTGAACCTTGATGCTCAGTATTTCCGAGNATACAT	2700
Qy	2701	TCAGAGTTTCAAAGCGCCAGTCATTTGCTCTCTGTTTCAAATCCAGGAAATTCGAGAGAGG	2760
Db	2701	TCAGAGTTTCAAAGCGCCAGTCATTTGCTCTCTGTTTCAAATCCAGGAAATTCGAGAGAGG	2760
Qy	2761	AATGTGCAACATTTCTGTGCCACTCTGGGGTCTTTAAAGAAACAAAGTCCAAAAGTCACTT	2820
Db	2761	AATGTGCAACATTTCTGTGCCACTCTGGGGTCTTTAAAGAAACAAAGTCCAAAAGTCACTT	2820
Qy	2821	TTGAATGTGAACAAAGGAGAGAAATCAAGGAAGATGATCTTAATCAAGCCTCTAC	2880
Db	2821	TTGAATGTGAACAAAGGAGAGAAATCAAGGAAGATGATGATCTTAATCAAGCCTCTAC	2880
Qy	2881	AGACAGTTAATATACATGACAGGCTTTCTGTTGGTTCAGAAAGATAAGCCAGTTGATA	2940
Db	2881	AGACAGTTAATATACATGACAGGCTTTCTGTTGGTTCAGAAAGATAAGCCAGTTGATA	2940
Qy	2941	ATGCCAAATGTAGTATCAAAAGGAGGCTCTAGGTTTGTCTATCATCTCAGTTACAGAGCA	3000
Db	2941	ATGCCAAATGTAGTATCAAAAGGAGGCTCTAGGTTTGTCTATCATCTCAGTTACAGAGCA	3000
Qy	3001	ACGAAATCGACTCATTTACTCCAAATAAACAATGGAATGATGTTTAAAGGAGCCAGCT	3060
Db	3001	ACGAAATCGACTCATTTACTCCAAATAAACAATGGAATGATGTTTAAAGGAGCCAGCT	3060
Qy	3061	CACACATTTTCCCATCAAGTCAATTTGTTAAAACTAAATGTAAGAAAAATCTGCTAGAGG	3120
Db	3061	CACACATTTTCCCATCAAGTCAATTTGTTAAAACTAAATGTAAGAAAAATCTGCTAGAGG	3120
Qy	3121	AAAACTTTGAGGAACATTTCAATGCTACCTGAAAGAGAAATGGGAAATGAGAACATTCGAA	3180
Db	3121	AAAACTTTGAGGAACATTTCAATGCTACCTGAAAGAGAAATGGGAAATGAGAACATTCGAA	3180
Qy	3181	GTACAGTGACCAATTTAGCCGCTAATAACATTAGAGAAATGTTTAAAGGAGCCAGCT	3240
Db	3181	GTACAGTGACCAATTTAGCCGCTAATAACATTAGAGAAATGTTTAAAGGAGCCAGCT	3240
Qy	3241	CAAGCAATATTAAATGAAGTAGGTTCCAGTAGTAAATGAAGTGGGCTCCAGTATTAAATGAAA	3300

Db 3341 CAAGCAATATTAATGAAGTAGGTTCCAGTACTAATGAAGTGGCTCCAGTATTAATGAAA 3300  
Qy TAGGTTCCAGTGATGAAGAAACATTCAGAGCAGAACTAGGTAGAGAAACAGAGGGCCAAAATTGA 3360  
Db TAGGTTCCAGTGATGAAGAAACATTCAGAGCAGAACTAGGTAGAGAAACAGAGGGCCAAAATTGA 3360  
Qy ATGCTATGCTTTAGATTTAGGGGTTTTGCAACTGAGGCTCTATAAAACAAAGTCTTCTCTGAAA 3420  
Db ATGCTATGCTTTAGATTTAGGGGTTTTGCAACTGAGGCTCTATAAAACAAAGTCTTCTCTGAAA 3420  
Qy GTAACTTGAAGCTTCCGAAATTAAGAAAGCAAGATATGAGAGTAGTTCAGACTGTTA 3480  
Db GTAACTTGAAGCTTCCGAAATTAAGAAAGCAAGATATGAGAGTAGTTCAGACTGTTA 3480  
Qy ATACAGATTTCTCTCCATATCTGATTTTCCAGATACTTTAGAACACGCTATGGAAGTAGTC 3540  
Db ATACAGATTTCTCTCCATATCTGATTTTCCAGATACTTTAGAACACGCTATGGAAGTAGTC 3540  
Qy ATGCATCTCAGGTTTGTCTGAGACACCTGATGACCTGTTAGATGATGTTGGAAGTAGTC 3600  
Db ATGCATCTCAGGTTTGTCTGAGACACCTGATGACCTGTTAGATGATGTTGGAAGTAGTC 3600  
Qy AAGATACCTAGTTTGTCTGAGAAATGACATTAAGGAAGTTCTGCTGTTTTAGGCAAAAGCG 3660  
Db AAGATACCTAGTTTGTCTGAGAAATGACATTAAGGAAGTTCTGCTGTTTTAGGCAAAAGCG 3660  
Qy TCCAGAGAGGAGAGCTTAGCAGAGGAGTCTGACCTTTTCCACCATACACATTTGCTCAGG 3720  
Db TCCAGAGAGGAGAGCTTAGCAGAGGAGTCTGACCTTTTCCACCATACACATTTGCTCAGG 3720  
Qy GTTACCGAAGAGGGCCCAAGAAATTAGAGTCTCTCAGAGAGAACTTATCTAGTGAGGATG 3780  
Db GTTACCGAAGAGGGCCCAAGAAATTAGAGTCTCTCAGAGAGAACTTATCTAGTGAGGATG 3780  
Qy AAGAGCTTCCCTGCTTCCAACTGTTTATTTGTTGTTAAAGTAAACAAATATATCTCTCAGT 3840  
Db AAGAGCTTCCCTGCTTCCAACTGTTTATTTGTTGTTAAAGTAAACAAATATATCTCTCAGT 3840  
Qy CTACTAGGCTAGCAGCTGCTGCTACCGAGTCTGCTCTAAGAAACACAGAGGAGAAATTTAT 3900  
Db CTACTAGGCTAGCAGCTGCTGCTACCGAGTCTGCTCTAAGAAACACAGAGGAGAAATTTAT 3900  
Qy TATCATTGAAGAAATAGCTTAAATGACTGCTGCTAAGAAAGTAAATTTGCAAGGAGCATCTC 3960  
Db TATCATTGAAGAAATAGCTTAAATGACTGCTAAGAAAGTAAATTTGCAAGGAGCATCTC 3960  
Qy AGGAACATCACTTAGTGAGGAAACAAATGTTCTGCTAGCTTGTCTTCTTCCACAGTGCA 4020  
Db AGGAACATCACTTAGTGAGGAAACAAATGTTCTGCTAGCTTGTCTTCTTCCACAGTGCA 4020  
Qy GTGAATTTGGAAGACTTGACTGCTCAATACAAACCCAGGATCCTTCTTGTAGTTGTTCTT 4080  
Db GTGAATTTGGAAGACTTGACTGCTCAATACAAACCCAGGATCCTTCTTGTAGTTGTTCTT 4080  
Qy CCAACAAATCAGGCTCAGCTGCTGAAAGCCAGGAGTTGCTGAGTGACAAAGAAATGG 4140  
Db CCAACAAATCAGGCTCAGCTGCTGAAAGCCAGGAGTTGCTGAGTGACAAAGAAATGG 4140  
Qy TTTTCCAGATGATGAAGAAAGAGGAAACGGGCTTTGGAAGAAATTAATCAAGAGAGCAAAAGCA 4200  
Db TTTTCCAGATGATGAAGAAAGAGGAAACGGGCTTTGGAAGAAATTAATCAAGAGAGCAAAAGCA 4200  
Qy TGGATTTCAACTTAGTGAGGAGGAGTCTGGGTGAGAGTGAAGAGGCTCTCTGAG 4260  
Db TGGATTTCAACTTAGTGAGGAGGAGTCTGGGTGAGAGTGAAGAGGCTCTCTGAG 4260  
Qy ACTGCTCAGGCTATCTCTCAGAGTGACATTTTAAACCACTCAGCAGAGGAGTACCATGC 4320  
Db ACTGCTCAGGCTATCTCTCAGAGTGACATTTTAAACCACTCAGCAGAGGAGTACCATGC 4320  
Qy AACATAAAGCTTCCAGCAGGAGAAATGGCTGAAGTGAAGCTGTGTAGAACAGC 4380  
Db AACATAAAGCTTCCAGCAGGAGAAATGGCTGAAGTGAAGCTGTGTAGAACAGC 4380

Db 4321 AACATAACCTGATTAAGCTCCAGCAGGAATGGCTGAAGCTAGAGCTGTGTAGAACAGC 4380  
Qy ATGGAGCCAGCCTTTAAACAGCTACCCCTTCCATCATTAAGTACTCTCTGCCCCTTGAGG 4440  
Db ATGGAGCCAGCCTTTAAACAGCTACCCCTTCCATCATTAAGTACTCTCTGCCCCTTGAGG 4440  
Qy ACCTGCGAAATCCAGAACAAAGCAGCATCAGAAAAGCAGTATTAACTTTCAGAGAAAGTA 4500  
Db ACCTGCGAAATCCAGAACAAAGCAGCATCAGAAAAGCAGTATTAACTTTCAGAGAAAGTA 4500  
Qy GTGAATACCTTATAAGCCAGAAATCCAGAGGCCCTTTCTGCTGACAAGTTTTCAGGTTGCTG 4560  
Db GTGAATACCTTATAAGCCAGAAATCCAGAGGCCCTTTCTGCTGACAAGTTTTCAGGTTGCTG 4560  
Qy CAGATAGTTCTTACAGTAAATAAAGAACCCAGAGTGGAAAGTCAATCCCTTCTTAAT 4620  
Db CAGATAGTTCTTACAGTAAATAAAGAACCCAGAGTGGAAAGTCAATCCCTTCTTAAT 4620  
Qy GCCCATCATTAGATGATAGTGGTACATGACAGTGTCTCTGGAGTCTTTCAGATAGAA 4680  
Db GCCCATCATTAGATGATAGTGGTACATGACAGTGTCTCTGGAGTCTTTCAGATAGAA 4680  
Qy ACTACCCATCTCAAGAGGAGCTCAATTAAGTGTGTTGATGTGGAGGACCAAGCTGGAAG 4740  
Db ACTACCCATCTCAAGAGGAGCTCAATTAAGTGTGTTGATGTGGAGGACCAAGCTGGAAG 4740  
Qy AGTCTGGGCCACACGATTTGACGGAACATCTTACTTGCACCAAGGCAAGATCTAGAGGAA 4800  
Db AGTCTGGGCCACACGATTTGACGGAACATCTTACTTGCACCAAGGCAAGATCTAGAGGAA 4800  
Qy CCCCTTACTGGAATCTGGAATCAGCCTCTTCTGATGACCCCTGAATCTGATCTCTCTG 4860  
Db CCCCTTACTGGAATCTGGAATCAGCCTCTTCTGATGACCCCTGAATCTGATCTCTCTG 4860  
Qy AAGCAGAGCCCCAGAGTCTGCTGTGTCACATACCATCTTCAACCTCTGCATTTGA 4920  
Db AAGCAGAGCCCCAGAGTCTGCTGTGTCACATACCATCTTCAACCTCTGCATTTGA 4920  
Qy AAGTTTCCCAATTTGAAAGTTGCAAGATCTGCCAGGGTCCAGCTGCTCTCATACTCTG 4980  
Db AAGTTTCCCAATTTGAAAGTTGCAAGATCTGCCAGGGTCCAGCTGCTCTCATACTCTG 4980  
Qy ATACTGCTGGGTATAATGCAATGGAAGAGTGTGAGCAGGAGGAGGCAAGATTTGACAG 5040  
Db ATACTGCTGGGTATAATGCAATGGAAGAGTGTGAGCAGGAGGAGGCAAGATTTGACAG 5040  
Qy CTTCAAAGAGAGGCTCAACAAAGAAATGTCATGGTGTGCTGCGCTGACCCAGAG 5100  
Db CTTCAAAGAGAGGCTCAACAAAGAAATGTCATGGTGTGCTGCGCTGACCCAGAG 5100  
Qy AATTTATGCTGCTGTAACAAGTTTCCAGAAAACACCATCACTTTAACTTAATCTAAATTA 5160  
Db AATTTATGCTGCTGTAACAAGTTTCCAGAAAACACCATCACTTTAACTTAATCTAAATTA 5160  
Qy CTGAAGAGCTACTCATGTTTATTAAGAAAACAGATGCTGAGTGTGTGTGAAACGACAC 5220  
Db CTGAAGAGCTACTCATGTTTATTAAGAAAACAGATGCTGAGTGTGTGTGAAACGACAC 5220  
Qy TGAATAATTTTCTAGGAATTTCCGGGAGGAAATGGGTAGTTAGCTATTTCTGGGTGACCC 5280  
Db TGAATAATTTTCTAGGAATTTCCGGGAGGAAATGGGTAGTTAGCTATTTCTGGGTGACCC 5280  
Qy AGTCTTTAAAGAAAGAAATGCTGAATGAGCATGATTTTGAAGTCAAGAGAGATGTGG 5340  
Db AGTCTTTAAAGAAAGAAATGCTGAATGAGCATGATTTTGAAGTCAAGAGAGATGTGG 5340  
Qy TCAATGGAAGAAACCAAGGCTCCAAAGCAGCAAGAGATCCAGGACAGAAAGATCT 5400  
Db TCAATGGAAGAAACCAAGGCTCCAAAGCAGCAAGAGATCCAGGACAGAAAGATCT 5400  
Qy TCAGGGGCTAGAAATCTGTTGCTATGGGCCCTTCAACCAATGCCCCACAGATCAACTGG 5460  
Db TCAGGGGCTAGAAATCTGTTGCTATGGGCCCTTCAACCAATGCCCCACAGATCAACTGG 5460

QY 5461 AATGATGGTACAGCTGTGTGCTCTCTGTGGTGAAGAGCTTTTCATCTACCCCTTG 5520  
DB 5461 AATGATGGTACAGCTGTGTGCTCTCTGTGGTGAAGAGCTTTTCATCTACCCCTTG 5520  
QY 5521 GCACAGGTGTCACCCCAATGTTGTTGTCAGCCAGATGCTGTCAGAGACAAATGGCT 5580  
DB 5521 GCACAGGTGTCACCCCAATGTTGTTGTCAGCCAGATGCTGTCAGAGACAAATGGCT 5580  
QY 5581 TCCATGCAATGGGCAGATGTCAGGACCTGTGTGACCCGAGAGTGGGTGTTGACA 5640  
DB 5581 TCCATGCAATGGGCAGATGTCAGGACCTGTGTGACCCGAGAGTGGGTGTTGACA 5640  
QY 5641 GTGTAGCACTTACCAAGTCCAGAGCTGGACACTTACCTGATACCCCGATCCCCACA 5700  
DB 5641 GTGTAGCACTTACCAAGTCCAGAGCTGGACACTTACCTGATACCCCGATCCCCACA 5700  
QY 5701 GCCACTACTGA 5711  
DB 5701 GCCACTACTGA 5711

## RESULT 14

AAC60794  
ID AAC60794 standard; cDNA; 5711 BP.

XX AAC60794;

XX 07-FEB-2001 (first entry)

XX Human BRCA1 (om12) nucleotide sequence SEQ ID NO:3.

XX Human; BRCA1; chromosome 17; 17q21; breast cancer; ovarian cancer;  
KW gene therapy; diagnosis; cytostatic; genetic susceptibility; mutation;  
KW polymorphism; identification; ss.

XX Homo sapiens.

XX US6130322-A.

XX 10-OCT-2000.

XX 06-MAY-1998; 98US-0074476.

XX 12-FEB-1996; 96US-0598591.

XX 12-DEC-1997; 97US-0798691.

XX (GENE-) GENE LOGIC INC.

XX Zeng B, Thurber D, Olson SJ, Alvares CP, Allen ACP, Murphy PD;

XX Critz BS;

XX WPI; 2000-646756/62.

XX P-PSDB; AAB24218.

XX New coding sequence of the human BRCA1 gene, i.e. BRCA1 (om12), useful  
PT in gene therapy, especially for preventing or treating breast or  
PT ovarian cancer, as well as for diagnosing or monitoring breast or  
PT ovarian cancer

XX Claim 1; Column 45-50; 56pp; English.

XX AAC60793 to AAC60795 encode the human BRCA1 (om1-3) proteins given in  
CC AAB24217 to AAB24219 respectively. BRCA1 is found on chromosome 17  
CC specifically to position 17q21. The BRCA1 (om12) coding sequence is  
CC sequence is useful in the present invention. The BRCA1 (om12) coding  
CC breast or ovarian cancer. It is also useful for preventing or treating  
CC breast or ovarian cancer. Furthermore, the BRCA1 (om12) coding sequence  
CC is useful for: (a) identifying individuals having BRCA1 gene mutations  
CC and having an increased genetic susceptibility to breast or ovarian  
CC cancer, or identifying a mutation that increases the genetic  
CC susceptibility to breast or ovarian cancer; (b) avoiding

CC misinterpretation of polymorphisms found in the BRCA1 gene; (c)  
CC determining the presence of a previously unknown mutation in the BRCA1  
CC gene; (d) probing a human sample of the BRCA1 gene by allele to determine  
CC the presence of either polymorphic alleles or mutations; and (e)  
CC performing diagnosis with a reagent derived from the BRCA1 (om1) cDNA  
CC sequence. AAC60796 to AAC60861 represent PCR primers for the BRCA1 gene,  
CC which are used in an example from the present invention.

XX SQ Sequence 5711 BP; 1953 A; 1098 C; 1277 G; 1383 T; 0 other;

Query Match 100.0%; Score 5709.4; DB 21; Length 5711;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 5710; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 AGCTCGCTGAGACTTCTCGACCCCGCACCAGGCTGTGGGGTTCTCAGATAACTGGGCC 60  
DB 1 AGCTCGCTGAGACTTCTCGACCCCGCACCAGGCTGTGGGGTTCTCAGATAACTGGGCC 60  
QY 61 CTTGGCTCAGGAGGCTTCAACCTCTGCTCTGGTAAAGTTCAATGGAAACAGAAAGAA 120  
DB 61 CTTGGCTCAGGAGGCTTCAACCTCTGCTCTGGTAAAGTTCAATGGAAACAGAAAGAA 120  
QY 121 TGGATTTATCTGCTCTTCGCTTGAAGAGTA CAAAATGCTATGATGATGAGAA 180  
DB 121 TGGATTTATCTGCTCTTCGCTTGAAGAGTA CAAAATGCTATGATGATGAGAA 180  
QY 181 TCTTAGAGTGTCCCATCTGCTGGAGTTGATCAAGGAACCTGTCCACAAGTGTGACC 240  
DB 181 TCTTAGAGTGTCCCATCTGCTGGAGTTGATCAAGGAACCTGTCCACAAGTGTGACC 240  
QY 241 ACATATTTTGCATAATTTTGCTGCTGAAACTTCTCAACCAAGAAAGAGGCTTTCACAGT 300  
DB 241 ACATATTTTGCATAATTTTGCTGCTGAAACTTCTCAACCAAGAAAGAGGCTTTCACAGT 300  
QY 301 GTCTTTTATGTAAGATGATATAACCAAAAGAGGCTTCAAGAAAGTACGAGATTTAGTC 360  
DB 301 GTCTTTTATGTAAGATGATATAACCAAAAGAGGCTTCAAGAAAGTACGAGATTTAGTC 360  
QY 361 AACTTGTGTAAGAGCTATTGAAATCATTTGCTTTTTCAGCTTGACACAGGTTTGAGT 420  
DB 361 AACTTGTGTAAGAGCTATTGAAATCATTTGCTTTTTCAGCTTGACACAGGTTTGAGT 420  
QY 421 ATGCAAAACAGCTATAATTTTGCATAAAAGGAAATAAATCTCTCTGAACATCTAAAGATG 480  
DB 421 ATGCAAAACAGCTATAATTTTGCATAAAAGGAAATAAATCTCTCTGAACATCTAAAGATG 480  
QY 481 AAGTTTCTATCATCCAAAGTATGGGCTACAGAAACCGTGCACAAAGAGCTTCTACAGAGTG 540  
DB 481 AAGTTTCTATCATCCAAAGTATGGGCTACAGAAACCGTGCACAAAGAGCTTCTACAGAGTG 540  
QY 541 AACCCGAAATCTCTCTTGCAGAAACAGCTCTCAGTGTCCAACCTCTTAACCTTGGAA 600  
DB 541 AACCCGAAATCTCTCTTGCAGAAACAGCTCTCAGTGTCCAACCTCTTAACCTTGGAA 600  
QY 601 CTGTGAGAACTCTGAGGACAAAGCAGCGATACAACTCAAAAGAGCTCTGTCTACATTG 660  
DB 601 CTGTGAGAACTCTGAGGACAAAGCAGCGATACAACTCAAAAGAGCTCTGTCTACATTG 660  
QY 661 AATTGGGATCTGATTCTTCTGAAGATACCGTTAATTAAGCAACTTATTGCAAGTGTGGAG 720  
DB 661 AATTGGGATCTGATTCTTCTGAAGATACCGTTAATTAAGCAACTTATTGCAAGTGTGGAG 720  
QY 721 ATCAAGAAATGTTACAAATCACCCCTCAAGGAACCGGATGAATCAGTTTGGATTCTG 780  
DB 721 ATCAAGAAATGTTACAAATCACCCCTCAAGGAACCGGATGAATCAGTTTGGATTCTG 780  
QY 781 CAAAAGAGGCTGCTGTGAAATTTTCTGAGACGATGTAAACAAATCTGAACATCATCAAC 840  
DB 781 CAAAAGAGGCTGCTGTGAAATTTTCTGAGACGATGTAAACAAATCTGAACATCATCAAC 840  
QY 841 CCAAGTAAATGATTTGAACACCACTGAGAAAGCGTGCAGCTGAGAGGCATCCAGAAAGT 900  
DB 841 CCAAGTAAATGATTTGAACACCACTGAGAAAGCGTGCAGCTGAGAGGCATCCAGAAAGT 900



Qy	901	ATCAGGTAGTTCGTGTTTCAAACCTTGCAATGTGGAGCCATGTGGCACAATAATCTCATGCCA	960
Db	901	ATCAGGTAGTTCGTGTTTCAAACCTTGCAATGTGGAGCCATGTGGCACAATAATCTCATGCCA	960
Qy	961	GCTCATTTACAGCATGAGAACGACAGTTTATTACTACCTAAAGACAGAAATGAATGTAGAAA	1020
Db	961	GCTCATTTACAGCATGAGAACGACAGTTTATTACTACCTAAAGACAGAAATGAATGTAGAAA	1020
Qy	1021	AGGCTGAATTCGTATAAAGCAAAACAGCCTGGCTTTAGCAAGGAGCAACATAACAGAT	1080
Db	1021	AGGCTGAATTCGTATAAAGCAAAACAGCCTGGCTTTAGCAAGGAGCAACATAACAGAT	1080
Qy	1081	GGGCTGGAAGTAAAGCAACATGTAAATGATAGGCGGACTCCAGGCACACAGAAAAAAGTAG	1140
Db	1081	GGGCTGGAAGTAAAGCAACATGTAAATGATAGGCGGACTCCAGGCACACAGAAAAAAGTAG	1140
Qy	1141	ATCTGAATGCTGATCCCTGTTGAGAGAAAAGAAATGGAATAAGCAGAAATCGCCATGCT	1200
Db	1141	ATCTGAATGCTGATCCCTGTTGAGAGAAAAGAAATGGAATAAGCAGAAATCGCCATGCT	1200
Qy	1201	CAGAGAAATCCTAGAGATACTGAAGATGTTCTTCGGATAACACTAAATAGCAGCAATTCAGA	1260
Db	1201	CAGAGAAATCCTAGAGATACTGAAGATGTTCTTCGGATAACACTAAATAGCAGCAATTCAGA	1260
Qy	1261	AAGTTAATGAGTGGTTTTCCAGAAAGTGAATGAACTGTTAGGTTCTGATGACTCACATGATG	1320
Db	1261	AAGTTAATGAGTGGTTTTCCAGAAAGTGAATGAACTGTTAGGTTCTGATGACTCACATGATG	1320
Qy	1321	GGGAGTCTGGAATCAAAATGCCAAAGTAGCTGATGTATTGGACGTTCTAAATGAGGTAGATG	1380
Db	1321	GGGAGTCTGGAATCAAAATGCCAAAGTAGCTGATGTATTGGACGTTCTAAATGAGGTAGATG	1380
Qy	1381	AATATTCTGGTTCTTCAGAGAAAAATAGACTTACTGGCCAGTGATCTCATGAGCCTTTAA	1440
Db	1381	AATATTCTGGTTCTTCAGAGAAAAATAGACTTACTGGCCAGTGATCTCATGAGCCTTTAA	1440
Qy	1441	TATGTAAGTGAAGAGTTCACCTCCAAATCAGTAGAGAGTAAATATTGAAGACAAATAAT	1500
Db	1441	TATGTAAGTGAAGAGTTCACCTCCAAATCAGTAGAGAGTAAATATTGAAGACAAATAAT	1500
Qy	1501	TTGGGAAAACTATCGGAAGAAGCAAGCCCTCCCAACTTAAGCCATGTAACTGAAAATC	1560
Db	1501	TTGGGAAAACTATCGGAAGAAGCAAGCCCTCCCAACTTAAGCCATGTAACTGAAAATC	1560
Qy	1561	TAATTTATAGAGCAATTTGTTACTAGGCCACAGATAAATACAGAGCGTCCCTCACAATA	1620
Db	1561	TAATTTATAGAGCAATTTGTTACTAGGCCACAGATAAATACAGAGCGTCCCTCACAATA	1620
Qy	1621	AAHTAAAGCGTAAAGGAGACCTACATCAGGCCCTTCATCCTGAGGATTTTATCAAGAAG	1680
Db	1621	AAHTAAAGCGTAAAGGAGACCTACATCAGGCCCTTCATCCTGAGGATTTTATCAAGAAG	1680
Qy	1681	CAGATTTGGCAGTTCAAAAGACTCCTGAAATGATAAATCAGGGAATCTAAACCAACGGAGC	1740
Db	1681	CAGATTTGGCAGTTCAAAAGACTCCTGAAATGATAAATCAGGGAATCTAAACCAACGGAGC	1740
Qy	1741	AGAATGGTCAAGTGATGAATTAATTAATAGTGGTCAATGAGATAAATAAGAGTCAATT	1800
Db	1741	AGAATGGTCAAGTGATGAATTAATTAATAGTGGTCAATGAGATAAATAAGAGTCAATT	1800
Qy	1801	CTATTCAGAAATGAGAAAAATCCTAAACCAATAGAAATCACTCGAAAAAGAAATCTGCTTTCA	1860
Db	1801	CTATTCAGAAATGAGAAAAATCCTAAACCAATAGAAATCACTCGAAAAAGAAATCTGCTTTCA	1860
Qy	1861	AAACGAAAGCTGAACCTTATAGCAGCAGTATAAGCAATATGGAATCGAAATTAATATCC	1920
Db	1861	AAACGAAAGCTGAACCTTATAGCAGCAGTATAAGCAATATGGAATCGAAATTAATATCC	1920
Qy	1921	ACAATTCAAAAGCACTTAAAGAAATAGCGTGAGGAGGAAGTCTTCTACAGGCAATATTC	1980
Db	1921	ACAATTCAAAAGCACTTAAAGAAATAGCGTGAGGAGGAAGTCTTCTACAGGCAATATTC	1980

QY	1981	ATGGCCTTGAACTAGTAGTGTAGTAGAGAAATCTAAGGCCACCCTAAATTGTGTATGTGAATTTGCAAA	2040
DB	1981	ATGGCCTTGAACTAGTAGTGTAGTAGAGAAATCTAAGGCCACCCTAAATTGTGTATGTGAATTTGCAAA	2040
QY	2041	TTGATAGTTGTTCTAGCAGGTGAAGAGATAAAGAAAAAAAAGTCAACCAAAATGCCAGTCA	2100
DB	2041	TTGATAGTTGTTCTAGCAGGTGAAGAGATAAAGAAAAAAAAGTCAACCAAAATGCCAGTCA	2100
QY	2101	GGCACAGCAGAAACTCTCAACTCATGTGAAGGTAAAGAACCTTGCNACTGGAGGCCAAGAA	2160
DB	2101	GGCACAGCAGAAACTCTCAACTCATGTGAAGGTAAAGAACCTTGCNACTGGAGGCCAAGAA	2160
QY	2161	GTAACAGGCCAAATGAAACAGACAAGTAAAAGACATGTGACAGTGTATCTTTCCCGAGAGCTGA	2220
DB	2161	GTAACAGGCCAAATGAAACAGACAAGTAAAAGACATGTGACAGTGTATCTTTCCCGAGAGCTGA	2220
QY	2221	AGTTAAACAAATGCACCTGGTCTCTTTTACTAAGTGTTCAAATACCAGTGAACCTTTAAAGAAT	2280
DB	2221	AGTTAAACAAATGCACCTGGTCTCTTTTACTAAGTGTTCAAATACCAGTGAACCTTTAAAGAAT	2280
QY	2281	TTGTCAATCTCTAGCCTTCCAAAGAGAGAAAAAGAGAAAACTAGAAAAAGTTTAAAGTGT	2340
DB	2281	TTGTCAATCTCTAGCCTTCCAAAGAGAGAAAAAGAGAAAACTAGAAAAAGTTTAAAGTGT	2340
QY	2341	CTAATAATGTGTAAGACCCCAAGATCTCATGTTAAGTGGAGAAAGGGTTTTGCAAACTG	2400
DB	2341	CTAATAATGTGTAAGACCCCAAGATCTCATGTTAAGTGGAGAAAGGGTTTTGCAAACTG	2400
QY	2401	AAAAGATCTGTAGAGATGACAGTATTTCACTGGTACCTGTGACTGTATTGGCACTCAGG	2460
DB	2401	AAAAGATCTGTAGAGATGACAGTATTTCACTGGTACCTGTGACTGTATTGGCACTCAGG	2460
QY	2461	AAAGTATCTCGTTACTGGAAAGTTAGCACTCTAGGGAAGGCAAAAAAGAACCAAAATAAT	2520
DB	2461	AAAGTATCTCGTTACTGGAAAGTTAGCACTCTAGGGAAGGCAAAAAAGAACCAAAATAAT	2520
QY	2521	GTGTGAGTCAAGTGTGCAGCACTTTGAAAAACCCCAAGGCACTAAATCATGTGTTGTTCCAAAG	2580
DB	2521	GTGTGAGTCAAGTGTGCAGCACTTTGAAAAACCCCAAGGCACTAAATCATGTGTTGTTCCAAAG	2580
QY	2581	ATAATAGNAATGACACAGAGGCTTTTAAAGTATCCATTGGGACATGAAGTTAACCAAGTC	2640
DB	2581	ATAATAGNAATGACACAGAGGCTTTTAAAGTATCCATTGGGACATGAAGTTAACCAAGTC	2640
QY	2641	GGGAAAACAAGCATAGAAATGGAAGAAAGTCAAATTGATGCTCAGTATTTTCGACAAATACAT	2700
DB	2641	GGGAAAACAAGCATAGAAATGGAAGAAAGTCAAATTGATGCTCAGTATTTTCGACAAATACAT	2700
QY	2701	TCAAGGTTTCAAAGCGCCAGTCACTTTGCTCTGTTTTCAAATCCAGGAAATGCAGAGAGG	2760
DB	2701	TCAAGGTTTCAAAGCGCCAGTCACTTTGCTCTGTTTTCAAATCCAGGAAATGCAGAGAGG	2760
QY	2761	AATGTGCAACATTTCTGTGCCACCTCTGGGTCTTTAAAGAAAACAAAGTCCAAAAGTCACTT	2820
DB	2761	AATGTGCAACATTTCTGTGCCACCTCTGGGTCTTTAAAGAAAACAAAGTCCAAAAGTCACTT	2820
QY	2821	TTGAATGTGAACAAAGGAAAGAAATCAAGGAAAGAAATGAGTCTAATATCAAGCCTGTAC	2880
DB	2821	TTGAATGTGAACAAAGGAAAGAAATCAAGGAAAGAAATGAGTCTAATATCAAGCCTGTAC	2880
QY	2881	AGACAGTTAATATCACTGCAGGCTTTTCTGTGTTGTCAGAAAGATAAGCCAGTTGATA	2940
DB	2881	AGACAGTTAATATCACTGCAGGCTTTTCTGTGTTGTCAGAAAGATAAGCCAGTTGATA	2940
QY	2941	ATGCCAAATGTAGTATCAAAAGGAGCTCTAGTTTTGTTCTATCATCTCAGTTTCAGAGGCA	3000
DB	2941	ATGCCAAATGTAGTATCAAAAGGAGCTCTAGTTTTGTTCTATCATCTCAGTTTCAGAGGCA	3000
QY	3001	ACGAACTGGACTCATTTACTCCAAATAAACAATGGACTTTTTACAAAACCCCATATCGTATAC	3060
DB	3001	ACGAACTGGACTCATTTACTCCAAATAAACAATGGACTTTTTACAAAACCCCATATCGTATAC	3060
QY	3061	CACCACCTTTTTCCCACATCAAGTCACTTTGTTAAAAACTAAATGTGAAGAAAAATCTGCTAGAGG	3120

[illegible]





Db 2821 TTGAATGTGAACAAAAGGAAGAAAATCAAGGAAGAATGAGTCTAATATCAAGCCTGTAC 2880  
Qy 2881 AGACAGTAAATATATCACTGCAGGCTTTCTCTGTGGTGTGCTCAGAAAGATAAGCCAGTTGATA 2940  
Db 2881 AGACAGTAAATATATCACTGCAGGCTTTCTCTGTGGTGTGCTCAGAAAGATAAGCCAGTTGATA 2940  
Qy 2941 ATGCGAAATGTAGTATCAAAAGGAGGCTCTAGGTTTGTCTATCATCTCAGTTTCAGAGGCA 3000  
Db 2941 ATGCGAAATGTAGTATCAAAAGGAGGCTCTAGGTTTGTCTATCATCTCAGTTTCAGAGGCA 3000  
Qy 3001 ACAGAACTGGACTCATTACTCCAAATAAATCAATGACATTTTACAAAAACCAATATCGTATAC 3060  
Db 3001 ACAGAACTGGACTCATTACTCCAAATAAATCAATGACATTTTACAAAAACCAATATCGTATAC 3060  
Qy 3061 CACCACATTTTCCCATCAAGTCAATTTGTTAAACTAAATGTAAAGAAAATCTGCTAGAGG 3120  
Db 3061 CACCACATTTTCCCATCAAGTCAATTTGTTAAACTAAATGTAAAGAAAATCTGCTAGAGG 3120  
Qy 3121 AAAAATTTGAGGAACATTCATATGTCACCTGAAAGAGAAATGGGAAATGAGAACATTTCCAA 3180  
Db 3121 AAAAATTTGAGGAACATTCATATGTCACCTGAAAGAGAAATGGGAAATGAGAACATTTCCAA 3180  
Qy 3181 GTACAGTGAGCACAAATAGCGGTAAATACATTAAGAGAAATGTTTAAAGGAGCCAGCT 3240  
Db 3181 GTACAGTGAGCACAAATAGCGGTAAATACATTAAGAGAAATGTTTAAAGGAGCCAGCT 3240  
Qy 3241 CAAGCAATATTAATGAAGTAGGTTCCAGTACTAATGAAGTGGGCTCCAGTATTAAATGAAA 3300  
Db 3241 CAAGCAATATTAATGAAGTAGGTTCCAGTACTAATGAAGTGGGCTCCAGTATTAAATGAAA 3300  
Qy 3301 TAGGTTCCAGTGATGAAAAACATTCAGAGCAATTCAGGTAGAAAACAGAGGGCCAAAATGGA 3360  
Db 3301 TAGGTTCCAGTGATGAAAAACATTCAGAGCAATTCAGGTAGAAAACAGAGGGCCAAAATGGA 3360  
Qy 3361 ATGCTATGCTTAGATTAGGGGTTTTGCAACCTGAGGTCTATAAACAAGTCTTCTCGGA 3420  
Db 3361 ATGCTATGCTTAGATTAGGGGTTTTGCAACCTGAGGTCTATAAACAAGTCTTCTCGGA 3420  
Qy 3421 GTAATGTGAACATCTCGAAATAAAGAGCAAGATATGAAGAGTAGTTAGTTCAGACTGTGA 3480  
Db 3421 GTAATGTGAACATCTCGAAATAAAGAGCAAGATATGAAGAGTAGTTAGTTCAGACTGTGA 3480  
Qy 3481 ATACAGATTTCTCTCCATATCTGATTTTCAGATAACTTAGAACACGCTATGGGAAGTAGTC 3540  
Db 3481 ATACAGATTTCTCTCCATATCTGATTTTCAGATAACTTAGAACACGCTATGGGAAGTAGTC 3540  
Qy 3541 ATGCACTCAGGTTGTTCTGAGACACCTGATGACCTGTAGATGATGTTGAATTAAGG 3600  
Db 3541 ATGCACTCAGGTTGTTCTGAGACACCTGATGACCTGTAGATGATGTTGAATTAAGG 3600  
Qy 3601 AAGTACTAGTTTGTGAAATGACATTAAGGAAAGTTCTGCTGTTTTAGCAAAAGCG 3660  
Db 3601 AAGTACTAGTTTGTGAAATGACATTAAGGAAAGTTCTGCTGTTTTAGCAAAAGCG 3660  
Qy 3661 TCCAGAGAGGAGAGCTTAGCAGGAGTCTAGCCCTTTTCAACCATACACATTTGGCTCAGG 3720  
Db 3661 TCCAGAGAGGAGAGCTTAGCAGGAGTCTAGCCCTTTTCAACCATACACATTTGGCTCAGG 3720  
Qy 3721 GTTACCGAAGAGGGGCCAAGAAAATAGAGTCTCAGAAAGAGAACTTATCTAGTGAGGATG 3780  
Db 3721 GTTACCGAAGAGGGGCCAAGAAAATAGAGTCTCAGAAAGAGAACTTATCTAGTGAGGATG 3780  
Qy 3781 AAGAGCTTCCCTGTTTCCAAACACTTGTATTTGGTAAAGTAAACAATATCTCTCAGT 3840  
Db 3781 AAGAGCTTCCCTGTTTCCAAACACTTGTATTTGGTAAAGTAAACAATATCTCTCAGT 3840  
Qy 3841 CTACTAGGCATAGCACCCCTGCTACCGAGTGTCTGCTTAAGAACACAGAGGAGAAATTTAT 3900  
Db 3841 CTACTAGGCATAGCACCCCTGCTACCGAGTGTCTGCTTAAGAACACAGAGGAGAAATTTAT 3900  
Qy 3901 TATCATTGAAGAATAGCTTAAATGATCTCAGTAACCGAGTAAATATGCGAAAGGATCTC 3960  
Db 3901 TATCATTGAAGAATAGCTTAAATGATCTCAGTAACCGAGTAAATATGCGAAAGGATCTC 3960

Qy 3961 AGGAAACATCACTTAGTGAGGAAACAAAATGTTTCTGTAGCTTGTCTTTCACAGTGCA 4020  
Db 3961 AGGAAACATCACTTAGTGAGGAAACAAAATGTTTCTGTAGCTTGTCTTTCACAGTGCA 4020  
Qy 4021 GTGAATTTGGAGACTTGACCTGCAAAATACAAACCCAGGATCCTTTCTTGAATGGTCTT 4080  
Db 4021 GTGAATTTGGAGACTTGACCTGCAAAATACAAACCCAGGATCCTTTCTTGAATGGTCTT 4080  
Qy 4081 CCAAAACAAATGAGGCACTCAGTCTGAAAGCCAGGAGTTGGTCTGAGTGACAAGGAAATGG 4140  
Db 4081 CCAAAACAAATGAGGCACTCAGTCTGAAAGCCAGGAGTTGGTCTGAGTGACAAGGAAATGG 4140  
Qy 4141 TTTTCAGATGATGAAGAAAGAGGAAACGGGCTTTGGAGAAAATAATCAAGAGAGCAAGCA 4200  
Db 4141 TTTTCAGATGATGAAGAAAGAGGAAACGGGCTTTGGAGAAAATAATCAAGAGAGCAAGCA 4200  
Qy 4201 TGGATTTCAAACTTAGGTGAAGCAGCATCTGGGTGTGAGAGTGAAACAAAGCGCTCTGAAG 4260  
Db 4201 TGGATTTCAAACTTAGGTGAAGCAGCATCTGGGTGTGAGAGTGAAACAAAGCGCTCTGAAG 4260  
Qy 4261 ACTGCTCAGGGCTATCTCTCAGAGTGACATTTTAAACCACTCAGCAGAGGATACCATGC 4320  
Db 4261 ACTGCTCAGGGCTATCTCTCAGAGTGACATTTTAAACCACTCAGCAGAGGATACCATGC 4320  
Qy 4321 AACATAAACCCTGATAAAGCTCCAGCAGGAAATGGCTGAACCTAGAAAGTGTGTTAGAACAGC 4380  
Db 4321 AACATAAACCCTGATAAAGCTCCAGCAGGAAATGGCTGAACCTAGAAAGTGTGTTAGAACAGC 4380  
Qy 4381 ATGGGAGCCAGCTTTTAAACAGCTACCTTTCCATCATAGTGACTCTCTGCCCTTGAGG 4440  
Db 4381 ATGGGAGCCAGCTTTTAAACAGCTACCTTTCCATCATAGTGACTCTCTGCCCTTGAGG 4440  
Qy 4441 ACCTGCCAAATCCAGAACAAAGCACATCAGAAAAAGCAGATTAACTTTCAGAAAAAGTA 4500  
Db 4441 ACCTGCCAAATCCAGAACAAAGCACATCAGAAAAAGCAGATTAACTTTCAGAAAAAGTA 4500  
Qy 4501 GTGAATAACCTTATAAGCCAGAAATCCAGAAAGCCTTTCTGTGACAAGTTTGAGGTGTCTG 4560  
Db 4501 GTGAATAACCTTATAAGCCAGAAATCCAGAAAGCCTTTCTGTGACAAGTTTGAGGTGTCTG 4560  
Qy 4561 CAGTAGTTCTACAGTAAATAAAGAACAGAGGTGGAAGGTCACTCCCTTCTTAAT 4620  
Db 4561 CAGTAGTTCTACAGTAAATAAAGAACAGAGGTGGAAGGTCACTCCCTTCTTAAT 4620  
Qy 4621 GCCCATCATTAGATGATAGTGTGACATGACAGTGTCTGTGGAGTCTTTCAGAAATAGAA 4680  
Db 4621 GCCCATCATTAGATGATAGTGTGACATGACAGTGTCTGTGGAGTCTTTCAGAAATAGAA 4680  
Qy 4681 ACTACCCATCTCAAGAGGAGCTCAATTAAGGTGTGATGTGGAGGAGCAACAGCTGGAAG 4740  
Db 4681 ACTACCCATCTCAAGAGGAGCTCAATTAAGGTGTGATGTGGAGGAGCAACAGCTGGAAG 4740  
Qy 4741 AGTCTGGGCCACAGATTTGACGAAACATCTTACTTGCAGGAGGAGATCTAGAGGAA 4800  
Db 4741 AGTCTGGGCCACAGATTTGACGAAACATCTTACTTGCAGGAGGAGATCTAGAGGAA 4800  
Qy 4801 CCCCTTACCTGGAATCTGGAATCAGCTCTTCTGTGATGACCTGAACTCTGATCTCTG 4860  
Db 4801 CCCCTTACCTGGAATCTGGAATCAGCTCTTCTGTGATGACCTGAACTCTGATCTCTG 4860  
Qy 4861 AAGACAGAGCCCGAGAGTCACTGCTGTGGCAACATACCACTTTCACACCTCTGCATTGA 4920  
Db 4861 AAGACAGAGCCCGAGAGTCACTGCTGTGGCAACATACCACTTTCACACCTCTGCATTGA 4920  
Qy 4921 AAGTTCCTCCAAATGAAAGTTGAGAAATCTGCCAGGGTCCAGTGTCTCATACTCTG 4980  
Db 4921 AAGTTCCTCCAAATGAAAGTTGAGAAATCTGCCAGGGTCCAGTGTCTCATACTCTG 4980  
Qy 4981 ATACTGTGGGTATTAATGCANTGGAAGAAAGTGTGAGCAGGAGAGCCAGAAATGACAG 5040  
Db 4981 ATACTGTGGGTATTAATGCANTGGAAGAAAGTGTGAGCAGGAGAGCCAGAAATGACAG 5040

QY 5041 CTTCAACAGAAAGGTCACAAAAGATGTCCATGGTGTGTCTGGCTGACCCAGAAAG 5100  
Db |||||  
QY 5041 CTTCAACAGAAAGGTCACAAAAGATGTCCATGGTGTGTCTGGCTGACCCAGAAAG 5100  
Db |||||  
QY 5101 AATTATGCTCGTGTAAGTTTGGCAGAAAACACCATCATCACTTTAACTAATCTAATTA 5160  
Db |||||  
QY 5101 AATTATGCTCGTGTAAGTTTGGCAGAAAACACCATCATCACTTTAACTAATCTAATTA 5160  
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QY 5161 CTGAAGAGACTACTCATGTTGTATGAAAACAGATGCTGAGTTTGTGTGTAACGGACAC 5220  
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QY 5161 CTGAAGAGACTACTCATGTTGTATGAAAACAGATGCTGAGTTTGTGTGTAACGGACAC 5220  
Db |||||  
QY 5221 TGAATAATTTTCTAGGAATTCGGGAGGAAATGGGTAGTTAGCTATTTCTGGGTGACCC 5280  
Db |||||  
QY 5221 TGAATAATTTTCTAGGAATTCGGGAGGAAATGGGTAGTTAGCTATTTCTGGGTGACCC 5280  
Db |||||  
QY 5281 AGTCTATTAAAGAAGAAAATGCTGAATGAGCATGATTTTGAAGTCAGAGGAGATGTGG 5340  
Db |||||  
QY 5281 AGTCTATTAAAGAAGAAAATGCTGAATGAGCATGATTTTGAAGTCAGAGGAGATGTGG 5340  
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QY 5341 TCAATGAAGAAACACCAAGGTCCTCAAGCGAGCAAGAGATCCACGACAGAAAGATCT 5400  
Db |||||  
QY 5341 TCAATGAAGAAACACCAAGGTCCTCAAGCGAGCAAGAGATCCACGACAGAAAGATCT 5400  
Db |||||  
QY 5401 TCAGGGGCTAGAAAATCTGTTGCTATGCGGCCCTTCACCAACATGCCACAGATCAACTGG 5460  
Db |||||  
QY 5401 TCAGGGGCTAGAAAATCTGTTGCTATGCGGCCCTTCACCAACATGCCACAGATCAACTGG 5460  
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QY 5461 AATGGATGTRACAGCTGTGGTCTTCTGTGGTGAAGGAGCTTTTCATCAACCTTG 5520  
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QY 5461 AATGGATGTRACAGCTGTGGTCTTCTGTGGTGAAGGAGCTTTTCATCAACCTTG 5520  
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QY 5521 GCACAGGTGTCACCCCAATTTGTTGTGTGAGCCAGATGCTGACAGAGGACAAATGGCT 5580  
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QY 5521 GCACAGGTGTCACCCCAATTTGTTGTGTGAGCCAGATGCTGACAGAGGACAAATGGCT 5580  
Db |||||  
QY 5581 TCCATGCAATTTGGCAGATGTGTGAGGCACCTGTGGTGACCCGAGAGTGGGTGTTGGACA 5640  
Db |||||  
QY 5581 TCCATGCAATTTGGCAGATGTGTGAGGCACCTGTGGTGACCCGAGAGTGGGTGTTGGACA 5640  
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QY 5641 GTGTAGCACTTACAGTCCAGAGCTGGACACCTACCTGATACCCAGATCCCCCACA 5700  
Db |||||  
QY 5641 GTGTAGCACTTACAGTCCAGAGCTGGACACCTACCTGATACCCAGATCCCCCACA 5700  
Db |||||  
QY 5701 GCCACTACTGA 5711  
Db |||||  
QY 5701 GCCACTACTGA 5711  
Db |||||

Search completed: December 14, 2003, 12:03:24  
Job time : 1347 secs



GenCore version 5.1.6  
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OM nucleic - nucleic search, using sw model

Run on: December 14, 2003, 09:36:27 ; Search time 10204 Seconds  
(without alignments)  
13602.789 Million cell updates/sec

Title: US-09-923-327A-263  
Perfect score: 5711  
Sequence: 1 agctcgtcgtgactctctg.....tccccacagccactactga 5711

Scoring table: IDENTITY NUC  
Gapop 10.0 , Gapext 1.0

Searched: 22781392 seqs, 1215238056 residues  
Total number of hits satisfying chosen parameters: 45562784

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database :  
EST:  
1: em\_estba:\*  
2: em\_esthum:\*  
3: em\_estlin:\*  
4: em\_estmu:\*  
5: em\_estov:\*  
6: em\_estpl:\*  
7: em\_estro:\*  
8: em\_hic:\*  
9: gb\_estcl:\*  
10: gb\_estcl2:\*  
11: gb\_hic:\*  
12: gb\_estcl3:\*  
13: gb\_estcl4:\*  
14: gb\_estcl5:\*  
15: em\_estfun:\*  
16: em\_estom:\*  
17: em\_gss\_hum:\*  
18: em\_gss\_inv:\*  
19: em\_gss\_pln:\*  
20: em\_gss\_vrt:\*  
21: em\_gss\_fun:\*  
22: em\_gss\_mam:\*  
23: em\_gss\_mus:\*  
24: em\_gss\_pro:\*  
25: em\_gss\_rnd:\*  
26: em\_gss\_phg:\*  
27: em\_gss\_vrt1:\*  
28: gb\_gsscl:\*  
29: gb\_gsscl2:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	2061.4	36.1	2101	11	BC012577 Homo sapi
2	2055.6	36.0	2090	11	BC030969 Homo sapi
3	1416.4	1578	11	BC038947	BC038947 Homo sapi
4	968.8	17.0	1919	11	AK086173 Mus muscu

Result No.	Score	Query Match	Length	ID	Description
5	863	15.1	962	13	BQ068830
6	841.4	14.7	1089	12	BM452288
7	810.2	14.2	845	9	AU122476
8	760.2	13.3	783	9	AU142729
9	746.4	13.1	933	13	BUI71200
10	738.8	12.9	899	13	BQ681276
11	734.6	12.9	878	13	BQ422380
12	706.2	12.4	856	13	BQ215100
13	698	12.2	856	13	BUI47444
14	687.6	12.0	747	12	BG777447
15	686.6	12.0	739	10	BF508987
16	686.4	12.0	702	9	AU125312
17	686.4	12.0	987	12	BM800251
18	658.6	11.5	900	10	BF791668
19	651.6	11.4	938	10	BG257190
20	639	11.2	675	9	AL704228
21	631	11.0	631	14	CB155501
22	617.6	10.8	921	10	BG178466
23	603.8	10.6	630	9	A1992040
24	593	10.4	906	13	BQ878445
25	593	10.4	909	13	BQ676829
26	593	10.4	922	13	BUI94336
27	592.6	10.4	933	13	BQ683955
28	591.4	10.4	724	9	A1915085
29	591.4	10.4	627	9	A1589028
30	589.4	10.3	800	10	BF794879
31	586	10.2	947	13	BQ679749
32	582.8	10.2	949	13	BUI55689
33	581	10.2	910	13	BQ677666
34	580.4	10.2	941	13	BUI63307
35	575	10.1	602	10	BE043993
36	548.2	9.6	638	12	BM042282
37	541.8	9.5	546	13	CB118225
38	535.2	9.4	638	10	BE264293
39	530	9.3	563	9	AW295197
40	528.6	9.3	585	10	AW968546
41	528	9.2	528	14	CB158976
42	516.4	9.0	666	10	AW968720
43	498.2	8.7	509	9	AW504244
44	493	8.6	894	13	BUI552955
45	492.8	8.6	509	10	BE018878

## ALIGNMENTS

RESULT 1  
LOCUS BC012577 2101 bp mRNA  
DEFINITION Homo sapiens, clone IMAGE:3996658, mRNA.  
ACCESSION BC012577.1 GI:15214876  
VERSION  
KEYWORDS  
SOURCE  
ORGANISM Homo sapiens (human)  
REFERENCE  
AUTHORS  
TITLE  
JOURNAL  
Submitted (15-AUG-2001) National Institutes of Health, Mammalian Gene Collection (MGC), Cancer Genomics Office, National Cancer Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590, USA

REMARK  
COMMENT  
NIH-MGC Project URL: <http://mgc.nci.nih.gov>  
Contact: MGC help desk  
Email: [cgapbs-remail.nih.gov](mailto:cgapbs-remail.nih.gov)  
Tissue Procurement: ATCC  
CDNA Library Preparation: CLONTECH Laboratories, Inc.  
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (ILNLT)  
DNA Sequencing by: Institute for Systems Biology  
<http://www.systemsbio.org>  
Contact: [amadan@systemsbio.org](mailto:amadan@systemsbio.org)

Oy	1	AGCTGCTGAGACTTCTCGAGACCCGACCAAGCTGTGGGGTTTCTCAGATTAAGTGGCC	60
Db	6	AGCTGCTGAGACTTCTCGAGACGGGGGA - CAGGCTGTGGGGTTTCTCAGATTAAGTGGCC	64
Oy	61	CCTGGGCTCAGAGAGGCTTTCAACCTCTGCTCTGGGTAAAGTTCAATGGAAACAGAAAGAA	120
Db	65	CCTGGGCTCAGAGAGGCTTTCAACCTCTGCTCTGGGTAAAGTTCAATGGAAACAGAAAGAA	124
Oy	121	TGATTTATTCGCTCTTGCGCGTTGAAAGATACAAATAGTCAATTAATCTATGGAGAAA	180
Db	125	TGATTTATTCGCTCTTGCGCGTTGAAAGATACAAATAGTCAATTAATCTATGGAGAAA	184
Oy	181	TCTTAGAGTGTCCATCTGTCTGAGTTGATCAAGAAACCTGTCTCAAAAGTGTACC	240
Db	185	TCTTAGAGTGTCCATCTGTCTGAGTTGATCAAGAAACCTGTCTCAAAAGTGTACC	244
Oy	241	ACATTTTTCGAAATTTTGCATGCTGAAACCTTTCACACAGAAAGAGGCTTCAACGT	300
Db	245	ACATTTTTCGAAATTTTGCATGCTGAAACCTTTCACACAGAAAGAGGCTTCAACGT	304
Oy	301	GTCCCTTATGTAAAGATATATTAACCAAAAGAGCTTCAAGAAAGTACGAGTTTATGTC	360
Db	305	GTCCCTTATGTAAAGATATATTAACCAAAAGAGCTTCAAGAAAGTACGAGTTTATGTC	364
Oy	361	AACTTGTGAAGACTATGAAATTCATTTGTGCTTTCAAGTTGACACAGTTTGGAGT	420
Db	365	AACTTGTGAAGACTATGAAATTCATTTGTGCTTTCAAGTTGACACAGTTTGGAGT	424
Oy	421	ATGCAACAGCTATATTTTGCAGAAAAAGAAATTAATCTCTCTGACATTTAAAGATG	480
Db	425	ATGCAACAGCTATATTTTGCAGAAAAAGAAATTAATCTCTCTGACATTTAAAGATG	484
Oy	481	AAAGTTTCATATCCAAAGTATGGGCTTCAAAAACCGGSCCAAAAAGCTTACAAGTGT	540
Db	485	AAAGTTTCATATCCAAAGTATGGGCTTCAAAAACCGGSCCAAAAAGCTTACAAGTGT	544
Oy	541	AAACCGAAATTCCTTCTTGCAGGAAACAGCTCTCAGTCCAACTCTTAACCTTGGAA	600
Db	545	AAACCGAAATTCCTTCTTGCAGGAAACAGCTCTCAGTCCAACTCTTAACCTTGGAA	604
Oy	601	CTGTGAGAACTCTGAGGACAAAGCAGCGGATPACAACCTCAAAAGAGCTGTCTPACAATTG	660
Db	605	CTGTGAGAACTCTGAGGACAAAGCAGCGGATPACAACCTCAAAAGAGCTGTCTPACAATTG	664
Oy	661	AATTGGGATCTGATTCCTTCTGAAGATTCOCGTTAATAAGGCAACTATTGCAAGTGTGGAG	720
Db	665	AATTGGGATCTGATTCCTTCTGAAGATTCOCGTTAATAAGGCAACTATTGCAAGTGTGGAG	724

QY	721	ATCAAGATTGTACAAATCCCCCTCAGGAACCGAGATGAAATCAGTTTGGATTCTG	780
Db	725	ATCAAGATTGTACAAATCCCCCTCAGGAACCGAGATGAAATCAGTTTGGATTCTG	784
QY	781	CAAAAAAGCGCTGTGTGAATTTTCTGAGAGGAGTGTAACAAAATCTGAACATCATCAAC	840
Db	785	CAAAAAAGCGCTGTGTGAATTTTCTGAGAGGAGTGTAACAAAATCTGAACATCATCAAC	844
QY	841	CCAGTAAATGATTTTGAAACACTGAGAAAGCTGCAGCTGAGAGGATCCAGAAAAGT	900
Db	845	CCAGTAAATGATTTTGAAACACTGAGAAAGCTGCAGCTGAGAGGATCCAGAAAAGT	904
QY	901	ATCAGGGAGTCTGTTTCAAACTTGACATGAGGCCATGTGGACAATCTCATGCA	960
Db	905	ATCAGGGAGTCTGTTTCAAACTTGACATGAGGCCATGTGGACAATCTCATGCA	964
QY	961	GCTCATTAACAGCATAGAACAGCAGTTTATTACTACATAAGACAGATGATGTAGAA	1020
Db	965	GCTCATTAACAGCATAGAACAGCAGTTTATTACTACATAAGACAGATGATGTAGAA	1024
QY	1021	AGGCTGAATTTCTGTAATPAAAGCAACAGCTGGCTTAGCAGAGCCACATPACGAT	1080
Db	1025	AGGCTGAATTTCTGTAATPAAAGCAACAGCTGGCTTAGCAGAGCCACATPACGAT	1084
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VERSION	BC030969.1	GI:21411299		
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ORGANISM	Eukaryota; Metazoa; Chordata; Craniata; Vertebrate; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.			
REFERENCE	1 (bases 1 to 2090)			
AUTHORS	Strausberg, R.			
TITLE	Direct Submission			
JOURNAL	Submitted (03-JUN-2002) National Institutes of Health, Mammalian Gene Collection (MGC), Cancer Genomics Office, National Cancer Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590, USA			
REMARK	NIH-MGC Project URL: <a href="http://mgc.nci.nih.gov">http://mgc.nci.nih.gov</a>			
COMMENT	Contact: MGC help desk Email: <a href="mailto:cgapdb-remail.nih.gov">cgapdb-remail.nih.gov</a> Tissue procurement: DCTD/DTF cDNA library preparation: CLONTECH Laboratories, Inc. cDNA library arrayed by: The I.M.A.G.E. Consortium (ILNL) DNA sequencing by: Sequencing Group at the Stanford Human Genome Center, Stanford University School of Medicine, Stanford, CA 94305 Web site: <a href="http://www.shgc.stanford.edu">http://www.shgc.stanford.edu</a> Contact: (Dickson, Mark) <a href="mailto:mcdopaxil.stanford.edu">mcdopaxil.stanford.edu</a> Dickson, M., Schmutz, J., Grimwood, J., Rodriguez, A., and Myers, R. M.			
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KEYWORDS   HTC.
SOURCE      Homo sapiens (human)
ORGANISM   Homo sapiens
REFERENCE   1 (bases 1 to 1578)
  AUTHORS   Strausberg, R.
  TITLE     Direct Submission
  JOURNAL   Submitted (01-NOV-2002) National Institutes of Health, Mammalian
            Gene Collection (MGC), Cancer Genomics Office, National Cancer
            Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
            USA
REMARK      NIH-MGC Project URL: http://mgc.nci.nih.gov
            Contact: MGC help desk
            Email: gcgaps-remail.nih.gov
            Tissue Procurement: ATCC
            cDNA Library Preparation: Life Technologies, Inc.
            cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
            DNA Sequencing by: National Institutes of Health Intramural
            Sequencing Center (NISC),
            Gaithersburg, Maryland.
            Web site: http://www.nisc.nih.gov/
            Contact: nisc_inq@nigr.nih.gov
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 REFERENCE 1  
 Carninci, P. and Hayashizaki, Y.  
 High-efficiency full-length cDNA cloning  
 Meth. Enzymol. 303, 19-44 (1999)  
 MEDLINE 99279253  
 PUBMED 10349636  
 REFERENCE 2  
 Carninci, P., Shibata, Y., Hayatsu, N., Sugahara, Y., Shibata, K., Itoh, M., Kono, H., Okazaki, Y., Muramatsu, M., and Hayashizaki, Y.  
 Normalization and subtraction of cap-trapper-selected cDNAs to prepare full-length cDNA libraries for rapid discovery of new genes  
 Genome Res. 10 (10), 1617-1630 (2000)  
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 PUBMED 11042159  
 REFERENCE 3  
 Shibata, K., Itoh, M., Aizawa, K., Nagaoka, S., Sasaki, N., Carninci, P., Kono, H., Akiyama, J., Nishi, K., Kitsumi, T., Tashiro, H., Itoh, M., Sumi, N., Ishii, Y., Nakamura, S., Hazama, M., Nishine, T., Harada, A., Yamamoto, R., Matsunoto, H., Sakaguchi, S., Ilegami, T., Kashiwagi, K., Fujiwaki, S., Inoue, K., Togawa, Y., Izawa, M., Ogata, E., Watanabe, M., Yoneda, Y., Ishikawa, T., Ozawa, K., Tanaka, T., Matsuzaki, S., Kawai, J., Okazaki, Y., Muramatsu, M., Inoue, Y., Kira, A., and Hayashizaki, Y.  
 RIKEN integrated sequence analysis (RISA) system--384-format sequencing pipeline with 384 multicapillary sequencer  
 Genome Res. 10 (11), 1757-1771 (2000)  
 MEDLINE 20530913  
 PUBMED 11076861  
 REFERENCE 4  
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Arakawa, T., Hara, A., Fukunishi, Y., Konno, H., Adachi, J., Fukuda, S.,  
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 and Hayashizaki, Y.  
 Functional annotation of a full-length mouse cDNA collection  
 Nature 409 (6821), 685-690 (2001)  
 2108560  
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 The FANTOM Consortium and the RIKEN Genome Exploration Research  
 Group Phase I & II Team.  
 Analysis of the mouse transcriptome based on functional annotation  
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 Nature 420, 563-573 (2002)  
 6 (bases 1 to 1919)  
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 Fukuda, S., Furuno, M., Hanagaki, T., Hara, A., Hashizume, M.,  
 Hayashida, K., Hayatsu, N., Hiramoto, K., Hirooka, T., Hirozane, T.,  
 Hori, F., Imotani, K., Ishii, Y., Itoh, M., Kagawa, I., Kasukawa, T.,  
 Katoh, H., Kawai, J., Kojima, Y., Kondo, S., Konno, H., Kouda, M.,  
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 Sogabe, Y., Tagami, M., Tagawa, A., Takahashi, F., Takaku-Akahira, S.,  
 Takeda, Y., Tanaka, T., Tomaru, A., Toya, T., Yasunishi, A.,  
 Muramatsu, M. and Hayashizaki, Y.  
 Direct Submission  
 Submitted (16-APR-2002) Yoshihide Hayashizaki, The Institute of  
 Physical and Chemical Research (RIKEN), Laboratory for Genome  
 Exploration Research Group, RIKEN Genomic Sciences Center (GSC),  
 RIKEN Yokohama Institute, 1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama,  
 Kanagawa 230-0045, Japan (E-mail: genome-res@gsc.riken.go.jp,  
 URL: http://genome.gsc.riken.go.jp/, Tel: 81-45-503-9222,  
 Fax: 81-45-503-9216)  
 cDNA library was prepared and sequenced in Mouse Genome  
 Encyclopedia Project of Genome Exploration Research Group in Riken  
 Genomic Sciences Center and Genome Science Laboratory in RIKEN.  
 Division of Experimental Animal Research in Riken contributed to  
 prepare mouse tissues.  
 Please visit our web site for further details.  
 URL: http://genome.gsc.riken.go.jp/  
 URL: http://fantom.gsc.riken.go.jp/  
 Location/Qualifiers  
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 BASE COUNT 616 a 401 c 462 g 440 t

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OY		4991	GTAATATCAATGGAAGAAGTGTGAGACAGGAGGAAGCCAGAAATTGACAGCTTCAAACA	5085
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Dd		795	TCTAGGAATTTGCGGAGGAAAAATGGGTAGTTAGTATTTCTGGGTGACCCAGTCTATTAA	854
OY		5291	AGAAAGAAAAATGCTGAATGAGCATGATTTTGAATCAGAGAGATGTGG--TCAATGA	5348
Dd		855	AGAAAGAAAAATGCTGAATGAGCATGATTTTGAATCAGAGAGATGTGGTCAATGGA	914
OY		5349	AGAAACCACCAAGATCTCAAAGCGAG	5373
Dd		915	AGAAACCACCAAGATCTCAAAGCGAG	939
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DEFINITION	AGENCOURT_6386302 NIH_MGC_72 Homo sapiens cDNA clone IMAGE:552666			
ACCESSION	BM452288			
VERSION	BM452288.1	GI:18501328		
KEYWORDS	EST.			
SOURCE	Homo sapiens (human)			
ORGANISM	Homo sapiens (human)			
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrate; Euteleostomi;			
AUTHORS	Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.			
TITLE	1 (bases 1 to 1089)			
JOURNAL	NIH-MGC http://mgc.nci.nih.gov/.			
COMMENT	National Institutes of Health, Mammalian Gene Collection (MGC) Unpublished			
	Contact: Robert Strausberg, Ph.D. Email: csapbe-remail.nih.gov Tissue Procurement: ATCC/DCTP cDNA Library Preparation: Life Technologies, Inc. cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNLN) DNA Sequencing by: Agencourt Bioscience Corporation Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LNLN at: <a href="http://image.llnl.gov">http://image.llnl.gov</a> Plate: LHAM12200 row: k column: 19 High quality sequence stop: 667. Location/Qualifiers 1..1089 /organism="Homo sapiens" /mol_type="mRNA" /db_xref="taxon:9606" /clone="IMAGE:552666" /tissue_type="melanotic melanoma" /lab_host="DH10B (phage-resistant)" /clone_id="NH MGC 72" /note="Organ: skin; Vector: pCMV-SPORT6; Site 1: NotI; Site 2: SalI; Cloned unidirectionally. primer: oligo dT. Average insert size 2 kb. Library constructed by Life Technologies."			
FEATURES				
source				

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Query Match	14.7%	Score 841.4;	DB 12;	Length 1089;	
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DB	73	GCTTGAATCTAGTAGTCAGTAGAAAATCTAAGCCCACTAATTGACTGAATTTGCAAAATTTGA	132		
QY	2045	TAGTTGTTCTAGCAGTGAAGAGATTAAGAAAAAAAGTACAAACCAATAGCCAGTCAGCA	2104		
DB	133	TAGTTGTTCTAGCAGTGAAGAGATTAAGAAAAAAAGTACAAACCAATAGCCAGTCAGCA	192		
QY	2105	CAGCAGAACTCTACACTCATGGAAGGTAAAGAACTGCAACTGAGCCCAAGAGAGATTA	2164		
DB	193	CAGCAGAACTCTACACTCATGGAAGGTAAAGAACTGCAACTGAGCCCAAGAGAGATTA	252		
QY	2165	CAAGCAAAATGAACAAGTAAAGCATGACAGATACCTTCCAGAGCTGAAGTT	2224		
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QY	2225	AACAAATGCACCTGGTCTCTTTTACTAAGTTCAAATACAGTGAACCTTAAAGAAATTTGT	2284		
DB	313	AACAAATGCACCTGGTCTCTTTTACTAAGTTCAAATACAGTGAACCTTAAAGAAATTTGT	372		
QY	2285	CAATCTTAGCTTCCAGAGAGAAAAAGAAAGAACTAGAAACAGTTAAAGTGTCTAA	2344		
DB	373	CAATCTTAGCTTCCAGAGAGAAAAAGAAAGAACTAGAAACAGTTAAAGTGTCTAA	432		
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QY	2645	AACAAGCATAGAAAT- GGAAGAAAAGTAACTTGATGCTCAGTATTTGGAGAAATCAATTCA	2703		
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Db	971 AACGAA 977
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LOCUS	AUI22476 845 bp mRNA linear EST 01-AUG-2002
DEFINITION	AUI22476 MAMMAL Homo sapiens cDNA clone MAMMAL002447 5', mRNA
ACCESSION	sequence.
VERSION	AUI22476
KEYWORDS	AUI22476.1 GI:10937746
SOURCE	EST.
ORGANISM	Homo sapiens (human)
REFERENCE	Homo sapiens
AUTHORS	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo. Ota, T., Nishikawa, T., Suzuki, Y., Ishii, S., Saito, K., Kawai, Y., Yamamoto, J., Wakematsu, A., Nakamura, Y., Nagai, T., Sugano, S. and Iisaga, T.
TITLE	HRI human cDNA project
JOURNAL	Unpublished
COMMENT	Contact: Takao Isogai Genomics Laboratory Helix Research Institute 1532-3 Yana, Kisarazu, Chiba 292-0812, Japan Tel: 81-438-52-3975 Fax: 81-438-52-3986 Email: genomics@hri.co.jp HRI human cDNA project; 5'- & 3'-end one pass sequencing; Helix Research Institute; cDNA library construction; Department of Virology, Institute of Medical Science, University of Tokyo, and Helix Research Institute. Location/Qualifiers 1. 845 /organism="Homo sapiens" /mol_type="mRNA" /db_xref="taxon:9606" /clone="MAMMAL002447" /issue_type="mammary gland" /clone_id="MAMMAL1" /note="Vector: pME18SFL3"
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3999	AGCTTGTCTTCTTCAAGTGCAGTGAATTTGAAGACTTGAAGTCAATATCAACACCCAG 4058
Db	181 AGCTTGTCTTCTTCAAGTGCAGTGAATTTGAAGACTTGAAGTCAATATCAACACCCAG 240
4059	GATCCTTCTTGAATGTTGTTCTTCCAAACAAATGAGGCAATGATGAGGAGGAGGATT 4118
Db	241 GATCCTTCTTGAATGTTGTTCTTCCAAACAAATGAGGCAATGATGAGGAGGAGGATT 300
4119	GGCTGAGTGCACAGAAATGTTTCAATGATGAAGAAAGAGAAACGGGCTTTGGAAGA 4178
Db	301 GGCTGAGTGCACAGAAATGTTTCAATGATGAAGAAAGAGAAACGGGCTTTGGAAGA 360
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VERSION				
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AUTHORS				
TITLE				
JOURNAL				
COMMENT				

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BASE COUNT      255 a      146 c      185 g      194 t      3 others
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Query Match      13.3%; Score 760.2; DB 9; Length 783;
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Db 61 TCTGCTGTTTTAGCAAAAGCGTCCAGAGAGAGAGTTCAGAGAGTCCCTGCTTC 120
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Db 121 ACCCATACACATTTGGCTCAGGGTTACCGAAGAGGGGCGAAGAAATTAGAGTCTCAGAA 180
QY 3759 GAGAACTTATCTAGAGAGATGAAGAGCTTCCCTGCTTCCAAACATTTGTTATTTGGTAAA 3818
Db 181 GAGAACTTATCTAGAGAGATGAAGAGCTTCCCTGCTTCCAAACATTTGTTATTTGGTAAA 240
QY 3819 GTAAACATATATACCTTCTCAGTCTACTAGAGCATACCGTTGCTACCGAGTGTCTCT 3878
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QY 3879 AAGAACACAGAGAGAAATTTATTTATCTAGTAAGAAATAGCTTAAATGACTGACGTAAACG 3938
Db 301 AAGAACACAGAGAGAAATTTATTTATCTAGTAAGAAATAGCTTAAATGACCGACGTAAACG 360
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QY 3999 AGCTTGTGTTCTTCCAGTGCAGTGAATTTGGAAGACTTGAAGTCAATATACAAACACCCAG 4058
Db 421 AGCTTGTGTTCTTCCAGTGCAGTGAATTTGGAAGACTTGAAGTCAATATACAAACACCCAG 480
QY 4059 GATCCTTTCTTGATTTGTTCTTCCAAACAAATGAGGATCAGTCTGAAAGCCAGGAGTT 4118
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Db 541 GGTCTGAGTGAACAAGAAATTTGGTTTCAATGATGAAGAAAGGAAACGGGCTTGGAAAGAA 600
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Db 601 AATATATCAAGAAAGCAAGCATGATTCAAACTTAGTGAAGAGCATCTGGGTGTGAG 660
QY 4239 AGTGAACAAGCGTCTTGAAAGACTGCTCAGGGCTATCTCTCAGAGTGAACATTTTAA-C 4297
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QY 4298 CACTCAGACAGAGGATACCATGCAACATTAACCTGTAAGCTCCAGAGAGAAATGGCTGA 4357
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RESULT 9
LOCUS      BUI71200      933 bp      mRNA      linear      EST 04-SEP-2002
DEFINITION AGNCOURT_7956206 NIH_MGC_72 Homo sapiens cDNA clone IMAGE:6161612
5', mRNA sequence.
ACCESSION      BUI71200
KEYWORDS      BUI71200.1 GI:22685184
SOURCE      EST. sapiens (human)
ORGANISM      Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
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REFERENCE      Mammalia; Eutheria; Primates; Catarrhini; Hominoidea; Homo.
AUTHORS      1 (bases 1 to 933)
TITLE      NIH-MGC http://mgi.nci.nih.gov/.
JOURNAL      National Institutes of Health, Mammalian Gene Collection (MGC)
COMMENT      Unpublished
Contact: Robert Strausberg, Ph.D.
Email: cgsbbs-remail.nih.gov
Tissue Procurement: ATCC/DCPD/DRP
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LIML)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LIML at:
http://image.liml.gov
plate: LIM13514 row: c column: 21
High quality sequence stop: 672.

FEATURES
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/note="Organ: skin; Vector: pCMV-SPORT6; Site 1: NciI; Site 2: SalI; Cloned unidirectionally. primer: oligo dt. Average insert size 2 kb. Library constructed by Life Technologies."

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ORIGIN

Query Match      13.1%; Score 746.4; DB 13; Length 933;
Best Local Similarity 98.3%; Pred. No. 5.8e-139;
Matches 765; Conservative 0; Mismatches 11; Indels 2; Gaps 1;

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Db 132 CTTCCTGATGACCTCTGAATCTGATCCTTCTGAGAGACAGAGCCGACAGTCACTCGTCT 191
QY 4889 TGGCAACATACCATCTTCAACCTCTGCAATTGAAAGTTCCCAATTGAAAGTTGAGCAATC 4948
Db 192 TGGCAACATACCATCTTCAACCTCTGCAATTGAAAGTTCCCAATTGAAAGTTGAGCAATC 251
QY 4949 TGCCAGGGGTCAGCTGCTGCTCATCTACTGATAGTCTGCGGTATATGCAATGAGAA 5008
Db 252 TGCCAGGGGTCAGCTGCTGCTCATCTACTGATAGTCTGCGGTATATGCAATGAGAA 311
QY 5009 AAGGTGAGCAGGGAGGAAGCCAGAAATTGACAGCTTCAACAGAAAGGTCACAAAGAAAT 5068
Db 312 AAGGTGAGCAGGGAGGAAGCCAGAAATTGACAGCTTCAACAGAAAGGTCACAAAGAAAT 371
QY 5069 GTCCATGGTGTGTCTGCGCTGACCCGAGAAATTTATGCTGCTGTAACAAGTTTGGCAG 5128
Db 372 GTCCATGGTGTGTCTGCGCTGACCCGAGAAATTTATGCTGCTGTAACAAGTTTGGCAG 431
QY 5129 AAAACACCAATCACTTTAATTAATCTAATTAATCTGAAAGAGACTCAATGTTTATGAA 5188
Db 432 AAAACACCAATCACTTTAATTAATCTAATTAATCTGAAAGAGACTCAATGTTTATGAA 491
QY 5189 AACAGATGCTGAGATTTGTGTGTGAACGAGACATGAAATATTTTCTAGAAATTTGGGAGG 5248
Db 492 AACAGATGCTGAGATTTGTGTGTGAACGAGACATGAAATATTTTCTAGAAATTTGGGAGG 551
QY 5249 AAATGAGGTAGTTAGTATTCTGGGTGACCCAGTCTATTAAAGAAAGAAATGCTGAA 5308
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Db      552  AAAATGGGTAGTACTATTTCTGGGTGACCCAGCTATTAAGAAAGAAAAATGCTGAA 611
Qy      5309  TGACACATGATTTTGAAGTCAGAGAGATGTGTCATATGGAAGAAACCCAGAGTCCAA 5368
Db      612  TGACACATGATTTTGAAGTCAGAGAGATGTGTCATATGGAAGAAACCCAGAGTCCAA 671
Qy      5369  GCGAGCAGAGAGATCCCGAGACAGAAAGATCTTCAGGGGCTAGAAATCTGTGCTATGG 5428
Db      672  GCGAGCAGAGAGATCCCGAGACAGAAAGATCTTCAGGGGCTAGAAATCTGTGCTATGG 731
Qy      5429  GCCCTTCACCAACATGCCACAG-ATCAACTGGAATGATGTACAGCTGTGTGG 5484
Db      732  GCCCTTCACCAACATGCCACAGANNATCATCTGGGAATGATGGGGTACAGCTGTGTG 789

RESULT 10
Bg681276 743 bp mRNA linear EST 01-MAY-2001
LOCUS 602627125F1 NCI_CGAP_Skn4 Homo sapiens cDNA clone IMAGE:4751887 5',
DEFINITION mRNA sequence.
ACCESSION Bg681276 GI:13912673
VERSION Bg681276.1
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE 1 (bases 1 to 743)
AUTHORS NIH-MGC http://mgc.nci.nih.gov/.
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished
COMMENT Contact: Robert Strusberg, Ph.D.
Email: cga@bbs-remail.nih.gov
Tissue Procurement: James Cleaver, M.D.
cDNA Library Preparation: Life Technologies, Inc.
DNA Library Arrayed by: The I.M.A.G.E. Consortium (LNLN)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LNLN at:
http://image.llnl.gov
Plate: LLM10609 row: a column: 08
High quality sequence stop: 741.
FEATURES
Source location/Qualifiers
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/clone="IMAGE:4751887"
/tissue_type="squamous cell carcinoma"
/lab_host="DH10B (TI phage-resistant)"
/clone_id="NCI_CGAP_Skn4"
/note="Organ: skin; Vector: pCMV-SPORT6; Site 1: NCI;
Site 2: Sail; Cloned unidirectionally. Primer: Oligo dT.
Average insert size 1.5kb. Library constructed by Life
Technologies. Note: this is a NCI_CGAP Library."
BASE COUNT 233 a 156 c 182 g 172 t
ORIGIN
Query Match 12.9%; Score 738.8; DB 10; Length 743;
Best Local Similarity 99.7%; Pred. No. 1.8e-137; Indels 0; Gaps 0;
Matches 740; Conservative 0; Mismatches 2;

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Db      121  TGAATCTGATCTCTTCGAGACAGAGCCCGAGCTCAGCTGTGTGGCAATACATC 180
Qy      4904  TTCAACCTCTGATTTGAAGTTCCCAATTGAAAGTTGACAGATCTGCCAGGGTCCAGC 4963
Db      181  TTCAACCTCTGATTTGAAGTTCCCAATTGAAAGTTGACAGATCTGCCAGGGTCCAGC 240
Qy      4964  TGTCTCTATCTACTGATCTGATCTGATCTGATCTGATCTGATCTGATCTGATCTG 5023
Db      241  TGTCTCTATCTACTGATCTGATCTGATCTGATCTGATCTGATCTGATCTGATCTG 300
Qy      5024  GAAGCCAGAAATTGACAGCTTCAACAGAAAGGTCACAAAGAAATGTCATGCTGCTC 5083
Db      301  GAAGCCAGAAATTGACAGCTTCAACAGAAAGGTCACAAAGAAATGTCATGCTGCTC 360
Qy      5084  TGGCTGACCCCGAAGAAATTATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 5143
Db      361  TGGCTGACCCCGAAGAAATTATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 420
Qy      5144  TTTAATCTATCTAATTTAATCTGAGAGACTACTCATGTTGTTATGAAACAGATGCT 5203
Db      421  TTTAATCTATCTAATTTAATCTGAGAGACTACTCATGTTGTTATGAAACAGATGCT 480
Qy      5204  TGTGTGTAACGACACTGAATATTTTCTAGAAATTCGGAGAGAAATGGTATGTTAG 5263
Db      481  TGTGTGTAACGACACTGAATATTTTCTAGAAATTCGGAGAGAAATGGTATGTTAG 540
Qy      5264  CTATTTCTGGGTGACCCAGTCTATTTAAAGAAAGAAATGCTGAATGACATGATTTGA 5323
Db      541  CTATTTCTGGGTGACCCAGTCTATTTAAAGAAAGAAATGCTGAATGACATGATTTGA 600
Qy      5324  AGTCAGAGAGATGTGTCATATGGAAGAAACCAACAGGTCCTCAAGCAGAGAGATTC 5383
Db      601  AGTCAGAGAGATGTGTCATATGGAAGAAACCAACAGGTCCTCAAGCAGAGAGATTC 660
Qy      5384  CCAGCAGAGAAAGATCTTCAGGGGCTAGAAATCTGTTGCTATGGCCCTTACCAACAT 5443
Db      661  CCAGCAGAGAAAGATCTTCAGGGGCTAGAAATCTGTTGCTATGGCCCTTACCAACAT 720
Qy      5444  GCCCAGATCACTGGAATGG 5465
Db      721  GCCCAGATCACTGGAATGG 742

RESULT 11
Bg422380 899 bp mRNA linear EST 23-MAY-2002
LOCUS Bg422380
DEFINITION AGENCOURT 7802085 NIH_MGC_92 Homo sapiens cDNA clone IMAGE:6042052
5', mRNA sequence.
ACCESSION Bg422380 GI:21117695
VERSION Bg422380.1
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE 1 (bases 1 to 899)
AUTHORS NIH-MGC http://mgc.nci.nih.gov/.
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished
COMMENT Contact: Robert Strusberg, Ph.D.
Email: cga@bbs-remail.nih.gov
Tissue Procurement: ATCC
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNLN)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LNLN at:
http://image.llnl.gov
Plate: LLM13280 row: n column: 05
High quality sequence stop: 597.
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Source location/Qualifiers
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/organism="Homo sapiens"

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/mol type="mRNA"
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Site 2: SalI; Cloned unidirectionally; oligo-dT primed.
Average insert size 2.5 kb. Library enriched for
full-length clones and constructed by Life Technologies.
Note: this is a NIH_MGC Library."
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Best Local Similarity 97.1%; Pred. No. 1.3e-136;
Matches 824; Conservative 0; Mismatches 11; Indels 14; Gaps 7;
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D 16 CAGGCTGTGGGTTTCTCAGATTAAGTGGGCGCTGCGCTCAGAGGCGCTTCAACCTCTGC 75
QY 90 TCTGGGTAAAGTTCAATTGAAACAGAAAGAAATGATTTATCTCTTCTGCGGTGAAGAA 149
D 76 TCTG-----GTTCATTTGAAACAGAAAGAAATGATTTATCTCTTCTGCGGTGAAGAA 129
QY 150 GTACAAATGTCAATTAAGTCAATGCAAGAAATCTTAAGTGTCCCATCTCTGTGAGCTTG 209
D 130 GTACAAATGTCAATTAAGTCAATGCAAGAAATCTTAAGTGTCCCATCTCTGTGAGCTTG 189
QY 210 ATCAAGAAAGCTGTCTCCACAAAGTGTACCAATATTTTGCATTTTGCATGCTGAA 269
D 190 ATCAAGAAAGCTGTCTCCACAAAGTGTACCAATATTTTGCATTTTGCATGCTGAA 249
QY 270 CTTCTCAACGAGAAAGAGGCGCTTCAAGTGTCTTATGTATGATATTAACCAAA 329
D 250 CTTCTCAACGAGAAAGAGGCGCTTCAAGTGTCTTATGTATGATATTAACCAAA 309
QY 330 AGGAGCCCAAGAAAGTACAGATTTAGTCACTGTGTGAAGAGCTTGAATATCACTT 389
D 310 AGGAGCCCAAGAAAGTACAGATTTAGTCACTGTGTGAAGAGCTTGAATATCACTT 369
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D 370 TGTGCTTTTCACTTGAACAGAGTTTGAATGCAACAGCTATTAATTTTGCATTTTGC 429
QY 450 GAAATTAATCTCTCTGAAATCTTAAAGATGAAGTTTCTATCATCAAAAGTATGGCTAC 509
D 430 GAAATTAATCTCTCTGAAATCTTAAAGATGAAGTTTCTATCATCAAAAGTATGGCTAC 489
QY 510 AGAAACCGTGCAGAAAGCTTCTACAGAGTGAACCCGAAATCTTCTCTTGCAGAAAC 569
D 490 AGAAACCGTGCAGAAAGCTTCTACAGAGTGAACCCGAAATCTTCTCTTGCAGAAAC 546
QY 570 AGTCTAGTGTCAACTCTCTCAACCTTGAAGTGTGAACCTTGAAGCAAGAGAGG 629
D 547 AGTCTAGTGTCAACTCTCTCAACCTTGAAGTGTGAACCTTGAAGCAAGAGAGG 606
QY 630 ATCAACCTCAAAAGAGCTGTGTCTCACTTGAATTTGGATCTGATTTCTTGAAGATAC 689
D 607 ATCAACCTCAAAAGAGCTGTGTCTCACTTGAATTTGGATCTGATTTCTTGAAGATAC 666
QY 690 GTTAAATAGGGAATTTATGAGTGTGGAGATCAAGATTTGTAACAATCAACCCCTCA 749
D 667 GTTAAATAGGGAATTTATGAGTGTGGAGATCAAGATTTGTAACAATCAACCCCTCA 726
QY 750 GGAACCA-GGGATGAATCAGTTGATTTGCAAAAAGGCTGC-TTGATATTTTCTG 807
D 727 GGAACCAAGGATGAATCAGTTGATTTGCAAAAAGGCTGTTTGATATTTTCTG 786
QY 808 AGACGATGTAAACA-ATATGAAATC-ATCAACCCAGTATATGA-TTTGAACCA 864
D 787 AGACGATGTAAACAATATGAAATC-ATCAACCCAGTATATGATTTTGAACCA 846

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QY 865 CTGGAAGC 873
D 847 CTGGAAGC 855

RESULT 12
LOCUS      BQ215100
DEFINITION BQ215100
ACCESSION  BQ215100
VERSION    BQ215100
KEYWORDS   EST.
SOURCE     Homo sapiens (human)
ORGANISM   Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniota; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
REFERENCE  1 (bases 1 to 878)
            NIH-MGC http://mgi.nci.nih.gov/.
            National Institutes of Health, Mammalian Gene Collection (MGC)
            Unpublished
            Contact: Robert Strausberg, Ph.D.
            Email: cga@b6-remail.nih.gov
            Tissue Procurement: ATCC/DCTP/DRP
            CDNA Library Preparation: Life Technologies, Inc.
            CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)
            DNA Sequencing by: Agencourt Bioscience Corporation
            Clone distribution: MGC clone distribution information can be
            found through the I.M.A.G.E. Consortium/LNL at:
            http://image.llnl.gov
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        Average insert size 2 kb. Library constructed by Life
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Query Match      12.4%; Score 706.2; DB 13; Length 878;
Best Local Similarity 98.8%; Pred. No. 6.6e-131;
Matches 754; Conservative 0; Mismatches 3; Indels 6; Gaps 4;
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D 13 CAGGCTGTGGGTTTCTCAGATTAAGTGGGCGCTGCGCTCAGAGGCGCTTCAACCTCTGC 72
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D 73 TCTGGGTAAAGTTCAATTGAAACAGAAAGAAATGATTTATCTCTTCTGCGGTGAAGAA 132
QY 150 GTACAAATGTCAATTAAGTCAATGCAAGAAATCTTAAGTGTCCCATCTGTGAGCTTG 209
D 133 GTACAAATGTCAATTAAGTCAATGCAAGAAATCTTAAGTGTCCCATCTGTGAGCTTG 192
QY 210 ATCAAGAAAGCTGTCTCCACAAAGTGTACCAATATTTTGCATTTTGCATGCTGAA 269
D 193 ATCAAGAAAGCTGTCTCCACAAAGTGTACCAATATTTTGCATTTTGCATGCTGAA 252
QY 270 CTTCTCAACGAGAAAGAGGCGCTTCAAGTGTCTTATGTATGAATATTAACCAAA 329
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/notes="Vector: pCMV-Sport6 (Life Technologies) ; Site 1:
      Note: Site 2: Salt; cDNA made by oligo-dT priming.

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RESULT 14					
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DEFINITION	6026645581 NIH_MGC_60 Homo sapiens CDNA clone IMAGE:4804551 5',				
	mRNA sequence.				

Accession	Version	KeyWords	Source	Organism	Reference	Authors	Title	Journal	Comment
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BC777447.1	1	GI:14047764	EST.	Homo sapiens (human)					
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				Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia; Euteleostomi; Mammalia; Eutheria; Primates; Catartida; Homiidae; Homo.					
				1 (bases 1 to 747)					
				NIH-MGC <a href="http://mhc.nci.nih.gov/">http://mhc.nci.nih.gov/</a> .					
				National Institutes of Health, Mammalian Gene Collection (MGC)					
				Unpublished					
				Contact: Robert Strausberg, Ph.D.					
				Email: <a href="mailto:cgabbs-r@mail.nih.gov">cgabbs-r@mail.nih.gov</a>					
				Tissue Procurement: DCTD/DRP					
				cDNA library Preparation: CLONETECH Laboratories, Inc.					
				cDNA library Arrayed by: The I.M.A.G.E. Consortium (ILNL)					
				DNA Sequencing by: Incyte Genomics, Inc.					
				Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/ILNL at:					
				<a href="http://image.llnl.gov">http://image.llnl.gov</a>					
				Place: LNCMI61 row: c column: 16					
				High quality sequence stop: 725.					
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				Query Match					
				Best Local Similarity 97.7%; Pred. No. 3.4e-127;					
				Matches 729; Conservative 0; Mismatches 14; Indels 3; Gaps 3					
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				3 AGCTCGTGAAGACTTCTCTGAGACGGGGGA-CAGGCTGTGGGGTTTCTCAGATTAACGGGCC 61					
				61 CCTGGCTCAGAGAGCCCTTCAACCTCTGCTCTGGGTTAAAGTTTCATTGGAACGAAAGAA 120					
				62 CCTGGCTCAGAGAGCCCTTCAACCTCTGCTCTGGGTTAAAGTTTCATTGGAACGAAAGAA 121					
				121 TGAATTAATCTGCTCTGCGCGTTGAAGAAAGTCAAAATGTCATTATGCTATGACGAGAAA 180					
				122 TGAATTAATCTGCTCTGCGCGTTGAAGAGTCAAAATGTCATTATGCTATGACGAGAAA 181					
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				241 ACATATTTTGCAGAAATTTTGCATGCTGAAACCTTCTCAACGAGAAAGGGCTTCAAGT 300					
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				301 GTCCCTTAATGTAAGATGATATTAACCAAAAGAGGCTCAAGAAAGTACGAGATTAGTC 360					
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Db	662	GAATTCGAGTCTGATTCCTTCT	GGAATACGTTAATAGCA	CTTAATTCAGTGT	GGG	721
Oy	719	AGATCAAGAAATTTGCAAA	TCAATCACC	744		
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RESULT 15						
BF508987/c						
LOCUS		739 bp	mRNA	linear	EST 06-DEC-2000	
DEFINITION		UI-H-B14-noc-b-06-0-UI.s1	NCI_CGAP_Sub8	Homo sapiens	cDNA clone	
IMAGE		3085787.3			mRNA sequence.	
ACCESSION		BF508987				
VERSION		BF508987.1			GI:11592285	
KEYWORDS		EST.				
SOURCE		Homo sapiens				
ORGANISM		Homo sapiens (human)				
REFERENCE						
AUTHORS		Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.				
TITLE		1 (bases 1 to 739)				
JOURNAL		NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.				
COMMENT		National Cancer Institute, Cancer Genome Anatomy Project (CGAP), Tumor Gene Index				
FEATURES		Unpublished				
SOURCE		Contact: Robert Strausberg, Ph.D.				
		Email: cgapsb-1@mail.nih.gov				
		The sequence contained an oligo-dT track that was present in the				
		oligonucleotide that was used to prime the synthesis of first				
		strand cDNA and therefore this may represent a bonafide poly A				
		tail. cDNA library Preparation: M.B. Soares lab clone distribution:				
		NCI-CGAP clone distribution information can be found through the				
		I.M.A.G.E. Consortium/ILND at:				
		www-bio.llnl.gov/bdrp/image/image.html				
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		POLYA-Yes.				
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		/note="Vector: pRT3D-Pac (Pharmacia) with a modified				
		polylinker; Site 1: Not I; Site 2: Eco RI; NCI CGAP Sub8				
		is a subtracted library derived from NCI CGAP Subs. The				
		NCI CGAP Subs library had 2.5 million recombinants. A				
		single-stranded DNA preparation of NCI CGAP Subs was used				
		as a tracer in a subtractive hybridization with a driver				
		comprising a pool of clones from NCI CGAP Subs (IMAGE				

clone ids 2732833-2737415, 3068040-3069191; 25% of the driver population), a pool of clones from NCI CGAP Sub4 (IMAGE clone ids 2723592-2729326; 25% of the driver population), NCI CGAP Sub6 (pool AIF-AJU, IMAGE ids 2728969-2733190; 25% of the driver population), and NCI CGAP Sub7 (IMAGE ids 3069192-3072238, 3081864-3084550; 25% of the driver population). Subtraction was performed as previously described [Bonaldi, Lennon & Soares (1996): Normalization and Subtraction: Two Approaches To Facilitate Gene Discovery. Genome Research 6, 791-806.

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ORIGIN

Query Match 12.0%; Score 686.6; DB 10; Length 739;  
Best Local Similarity 99.1%; Pred.No. 5.3e-127;  
Matches 689; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

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DB 638 AAAAGTGAAAGTCTCACTCCAAATCAGTAGAGTAAATATTGAACAAATATTTGGG 579

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DB 578 AAAAACCCTATCGGAAAGAGGCAAGCTCCCACTTAAGCCATGTAAGTAAATCTAATT 519

QY 1566 ATAGAGACATTTGTTACTGAGGCAAGATTAATACAGAGCGGCCCTCCCAATTAATTA 1625  
DB 518 ATAGAGACATTTGTTACTGAGGCAAGATTAATACAGAGCGGCCCTCCCAATTAATTA 459

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QY 1686 TTGGCAGTTCAAAAAGACTCTGAAATGATTAATCAGGGACTAACCAACGAGCAGAT 1745  
DB 398 TTGGCAGTTCAAAAAGACTCTGAAATGATTAATCAGGGACTAACCAACGAGCAGAT 339

QY 1746 GGTCAAGTATGATTAATTAATAGTGTGATGAAATTAACAAAGGTGATTTCTATT 1805  
DB 338 GGTCAAGTATGATTAATTAATAGTGTGATGAAATTAACAAAGGTGATTTCTATT 279

QY 1806 CAGATGAGAAAAATCTTAACCAATAGATCACTCGAAAAAGAAATCTGCTTTCAAAAG 1865  
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DB 218 AAAGCTGAACCTATAGCAGAGATTAAGCAATATGAACTCGAATTAATATTCACAAT 159

QY 1926 TCAAAAGCACTTAATAAAGATAGGCTGAGAGAAAGTCTTCTACCAAGCATATTCATGCG 1985  
DB 158 TCAAAAGCACTTAATAAAGATAGGCTGAGAGAAAGTCTTCTACCAAGCATATTCATGCG 99

QY 1986 CTTGAACCTAGTAGTCAGTAGAAATCTAAGCCCACTTAATGTAAGTGAATGCAATTTGAT 2045  
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GenCore version 5.1.6  
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## OM nucleic - nucleic search, using sw model

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7243.503 Million cell updates/sec

Title: US-09-923-327A-263

Perfect score: 5711  
Sequence: 1 agtcgcgtgactctctgg.....tccccacagcactactga 5711

Scoring table: IDENTITY NUC

Gapop 10.0 , Gapext 1.0

Searched: 569978 seqs, 220691566 residues

Total number of hits satisfying chosen parameters: 1139956

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Issued Patents NA:\*

- 1: /cgnt\_6/ptodata/2/ina/5A.COMB.seq:\*
- 2: /cgnt\_6/ptodata/2/ina/5B.COMB.seq:\*
- 3: /cgnt\_6/ptodata/2/ina/6A.COMB.seq:\*
- 4: /cgnt\_6/ptodata/2/ina/6B.COMB.seq:\*
- 5: /cgnt\_6/ptodata/2/ina/PCtUS.COMB.seq:\*
- 6: /cgnt\_6/ptodata/2/ina/backfile1.seq:\*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	5711	100.0	5711	1	US-08-598-591-1 Sequence 1, Appli
2	5711	100.0	5711	1	US-08-798-691-1 Sequence 1, Appli
3	5711	100.0	5711	3	US-08-825-487A-1 Sequence 1, Appli
4	5711	100.0	5711	3	US-08-074-476-1 Sequence 1, Appli
5	5709.4	100.0	5711	1	US-08-798-691-5 Sequence 5, Appli
6	5709.4	100.0	5711	3	US-08-825-487A-5 Sequence 5, Appli
7	5709.4	100.0	5711	3	US-08-074-476-3 Sequence 3, Appli
8	5701.4	99.8	5711	1	US-08-798-691-3 Sequence 3, Appli
9	5701.4	99.8	5711	3	US-08-825-487A-3 Sequence 3, Appli
10	5701.4	99.8	5711	3	US-08-074-476-5 Sequence 5, Appli
11	5699.8	99.8	5711	2	US-08-658-322-1 Sequence 1, Appli
12	5699.8	99.8	5712	2	US-08-603-753D-1 Sequence 1, Appli
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16	5699.8	99.8	5914	1	US-08-480-784-1 Sequence 1, Appli
17	5699.8	99.8	5914	1	US-08-483-553-1 Sequence 1, Appli
18	5699.8	99.8	5914	1	US-08-487-002-1 Sequence 1, Appli
19	5699.8	99.8	5914	1	US-08-483-554B-1 Sequence 1, Appli
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21	5699.8	99.8	5914	3	US-08-850-727-1 Sequence 1, Appli
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24	5699.8	99.8	5914	5	PCT-US95-10220-1 Sequence 1, Appli
25	5698.2	99.8	5711	1	US-08-425-061-4 Sequence 10, Appli
26	5698.2	99.8	5711	1	US-08-425-061-10 Sequence 4, Appli
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38	5685.8	99.6	5709	1	US-08-425-061-7 Sequence 7, Appli
39	5685.8	99.6	5709	1	US-08-425-061-8 Sequence 8, Appli
40	5685.8	99.6	5709	1	US-08-425-061-9 Sequence 9, Appli
41	5685.8	99.6	5709	1	US-08-825-886-2 Sequence 2, Appli
42	5685.8	99.6	5709	1	US-08-825-886-7 Sequence 7, Appli
43	5685.8	99.6	5709	1	US-08-825-886-8 Sequence 8, Appli
44	5685.8	99.6	5709	1	US-08-825-886-9 Sequence 9, Appli
45	5685.8	99.6	5709	4	US-08-989-890-2 Sequence 2, Appli

## ALIGNMENTS

RESULT 1  
US-08-598-591-1  
; Sequence 1, Application US/08598591  
; Patent No. 5654155  
; GENERAL INFORMATION:  
; APPLICANT: Allen, Antoinette C.  
; APPLICANT: Alvarez, Christopher P.  
; APPLICANT: Critz, Brenda S.  
; APPLICANT: Murphy, Patricia D.  
; APPLICANT: Olson, Sheri J.  
; APPLICANT: Scheiter, Denise B.  
; APPLICANT: Zeng, Bin  
; TITLE OF INVENTION: A Consensus Sequence of the Human BRCA1 Gene  
; Patent No. 5654155  
; NUMBER OF SEQUENCES: 74  
; CORRESPONDENCE ADDRESSES:  
; ADDRESSEE: BURNS, DOANE, SWECKER & MATHIS  
; STREET: 699 Prince St.  
; CITY: Alexandria  
; STATE: VA  
; COUNTRY: USA  
; ZIP: 22314  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patentin Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/598,591  
; FILING DATE: herewith  
; CLASSIFICATION: 435  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Swecker, Robert S.  
; REGISTRATION NUMBER: 19,885  
; REFERENCE/DOCKET NUMBER: 020160-282  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 703-836-6620  
; TELEFAX: 703-836-2021  
; INFORMATION FOR SEQ ID NO: 1:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 5711 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: not relevant  
; TOPOLOGY: linear  
; MOLECULE TYPE: cDNA  
; ORIGINAL SOURCE:  
; ORGANISM: Homo sapiens  
; STRAIN: BRCA1  
; POSITION IN GENOME:  
; CHROMOSOME/SEGMENT: 17

MAP POSITION: 17q21  
US-08-598-591-1

Query Match 100.0%; Score 5711; DB 1; Length 5711;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 5711; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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DB 61 CTTGGGCTCAGAGAGGCTTCAACCTCTGCTGGTAAAGTTCAITGGAAACAGAAAGAAA 120
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Db 2401 AAAGATCTGTAGAGATGACGATTTTCACTGTTACTGTTACTGATTTATGCACTCAG 2460  
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ORGANISM: Homo sapiens  
STRAIN: BRCA1  
POSITION IN GENOME:  
CHROMOSOME/SEGMENT: 17  
MAP POSITION: 17q21  
US-08-798-691-1

Query Match 100.0%; Score 5711; DB 1; Length 5711;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 5711; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AGCTGCTGAGACTTCTGAGACCCCGCACCGAGCTGTGGGTTTCTCAGATTAAGTGGCC 60  
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QY 241 ACATATTTTGCAGATTTTGCATGCTGAAACTTCTCAACGAGAAAGAGGCTTCAAGT 300  
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Qy      4921 AAGTCCCAATTTGAAAGTTGACAGATCTGCGCAGAGTCCAGCTGCTCTCATCTACTG 4980
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Db      4981 ATACTGCTGGGTATATGCAATGGAAGAAAGTGTGAGCAGAGGAGAAAGCAGAAATTTGACG 5040
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RESULT 3
US-08-825-487A-1
; Sequence 1, Application US/08825487A
; Patent No. 6048689
; GENERAL INFORMATION:
; APPLICANT: Murphy, Patricia D.
; APPLICANT: White, Marga B.
; TITLE OF INVENTION: METHODS FOR IDENTIFYING VARIATIONS IN POLYNUCLEOTIDE SEQUENCE
; NUMBER OF SEQUENCES: 110
; CORRESPONDENCE ADDRESS:
; ADDRESS: Howrey & Simon
; STREET: 1299 Pennsylvania Avenue., N.W.
; CITY: Washington,
; STATE: DC
; COUNTRY: USA
; ZIP: 20004
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: IBM PC compatible
; SOFTWARE: Patent Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/825,487A
; FILING DATE: 28-MAR-1997
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/US98/060002
; FILING DATE: 26-Mar-1998
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Albert P. Halluin
; REGISTRATION NUMBER: 25,227
; REFERENCE/DOCKET NUMBER: 05371.0012.999
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 650-463-8100
; TELEFAX: 650-463-8400
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 5711 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: not relevant
; TOPOLOGY: linear

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MOLECULE TYPE: cDNA  
ORIGINAL SOURCE:  
ORGANISM: Homo sapiens  
STRAIN: BRCA1  
POSITION IN GENOME:  
CHROMOSOME/SEGMENT: 17  
MAP POSITION: 17q21  
US-08-825-487A-1

Query Match 100.0%; Score 5711; DB 3; Length 5711;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 5711; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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RESULT 4  
US-09-074-476-1  
Sequence 1, Application US/09074476  
Patent No. 6130322  
GENERAL INFORMATION:  
APPLICANT: Murphy, Patricia D.  
APPLICANT: Allen, Antoinette C.  
APPLICANT: Alvarez, Christopher P.  
APPLICANT: Cirlitz, Brenda S.  
APPLICANT: Olson, Sheri J.  
APPLICANT: Thurber, Denise  
APPLICANT: Zeng, Bin  
TITLE OF INVENTION: Coding Sequences of the Human  
TITLE OF INVENTION: BRCA1 Gene  
NUMBER OF SEQUENCES: 72  
CORRESPONDENCE ADDRESSES:  
ADDRESSEE: Howrey & Simon  
STREET: 1299 Pennsylvania Avenue N. W.  
CITY: Washington  
STATE: DC  
COUNTRY: USA  
ZIP: 20004  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/074,476  
FILING DATE:  
CLASSIFICATION:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 09/074,453  
FILING DATE:  
ATTORNEY/AGENT INFORMATION:  
NAME: Albert P. Halluin  
REGISTRATION NUMBER: 25,227  
REFERENCE/DOCKET NUMBER: 5371.34.US01  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 650-463-8109

TELEFAX: 650-463-8400  
INFORMATION FOR SEQ ID NO: 1:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 5711 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: not relevant  
TOPOLOGY: linear  
MOLECULE TYPE: cDNA  
ORIGINAL SOURCE:  
ORGANISM: Homo sapiens  
STRAIN: BRC1 (omit)  
POSITION IN GENOME:  
CHROMOSOME/SEGMENT: 17  
MAP POSITION: 17q21  
US-09-074-476-1

Query Match 100.0%; Score 5711; DB 3; Length 5711;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 5711; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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RESULT 5  
 US-08-798-691-5  
 Sequence 5, Application US/08798691  
 Patent No. 5750400  
 GENERAL INFORMATION:  
 APPLICANT: Murphy, Patricia D.  
 APPLICANT: Allen, Antoinette C.  
 APPLICANT: Alvarez, Christopher P.  
 APPLICANT: Critz, Brenda S.  
 APPLICANT: Olson, Sheri J.  
 APPLICANT: Schebler, Denise B.  
 APPLICANT: Zeng, Bin  
 TITLE OF INVENTION: Coding Sequences of the Human  
 TITLE OF INVENTION: BRCA1 Gene  
 NUMBER OF SEQUENCES: 72  
 CORRESPONDENCE ADDRESS:  
 ADDRESSEE: ONCOMED  
 STREET: 200 Perry Parkway  
 CITY: Gaitthersberg  
 STATE: MD  
 COUNTRY: USA  
 ZIP: 20877  
 COMPUTER READABLE FORM:  
 MEDIUM TYPE: Floppy disk  
 COMPUTER: IBM PC compatible  
 OPERATING SYSTEM: PC-DOS/MS-DOS  
 SOFTWARE: Patent In Release #1.0, Version #1.30  
 CURRENT APPLICATION DATA:  
 APPLICATION NUMBER: US/08/798,691  
 FILING DATE: 12-Feb-97  
 CLASSIFICATION: 435  
 ATTORNEY/AGENT INFORMATION:  
 NAME: Thomas Gallegos





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[illegible]

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Db      5701 GCCACTACTGA 5711

RESULT 6
US-08-825-487A-5
; Sequence 5, Application US/08825487A
; Patent No. 6048689
; GENERAL INFORMATION:
; APPLICANT: Murphy, Patricia D.
; APPLICANT: White, Marga B.
; TITLE OF INVENTION: METHODS FOR IDENTIFYING VARIATIONS IN POLYNUCLEOTIDE SEQUENCES
; NUMBER OF SEQUENCES: 110
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Howrey & Simon
; STREET: 1299 Pennsylvania Avenue, N.W.
; CITY: Washington,
; STATE: DC
; COUNTRY: USA
; ZIP: 20004
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/825,487A
; FILING DATE: 28-MAR-1997
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/US98/060002
; FILING DATE: 26-Mar-1998
; CLASSIFICATION: 435

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QY	1801	CTATTGAGATGAGAAAAATCTTAACCAATATGAAATCACTGAGAAAAAGAAATCTGCTTCA	1860
Db	1801	CTATTGAGAAATGAGAAAAATCTTAACCAATATGAAATCACTGAGAAAAAGAAATCTGCTTCA	1860
QY	1861	AAAGCAAAAGCTGAACTTAATTAAGCAGACAGATATAGCAATATGGAAGTCTGAAATTAATATCC	1920
Db	1861	AAACGAAAGCTGAACCTTAATTAAGCAGACAGATATAGCAATATGGAAGTCTGAAATTAATATCC	1920
QY	1921	ACAAATTCAAAAGCACCCTAAAAAGAAATAGGCTGAGAGGAAGTCTTCTACAGCAATATTC	1980
Db	1921	ACAAATTCAAAAGCACCCTAAAAAGAAATAGGCTGAGAGGAAGTCTTCTACAGCAATATTC	1980
QY	1981	ATGCGCTTGAACCTAGTACTCAGTAGAAATCTPAAGCCCACTAATTTGTAATGCAATTCGAAA	2040
Db	1981	ATGCGCTTGAACCTAGTACTCAGTAGAAATCTPAAGCCCACTAATTTGTAATGCAATTCGAAA	2040
QY	2041	TTGATAGTGTCTCTAGCAGTGAAGAGATPAAGAAAAAAGATGACAAACCAATATGCAAGTCA	2100
Db	2041	TTGATAGTGTCTCTAGCAGTGAAGAGATPAAGAAAAAAGATGACAAACCAATATGCAAGTCA	2100
QY	2101	GGCACAGCAGAAACCTTACAACTCAATGAGAAAGTAAAGAAACCTTGCACTGAGCCCAAGAGA	2160
Db	2101	GGCACAGCAGAAACCTTACAACTCAATGAGAAAGTAAAGAAACCTTGCACTGAGCCCAAGAGA	2160
QY	2161	GTAACAAAGCAAAATGAAACAGACAGTAAGAAAGACATGACGTATCTTCCCAAGCTGA	2220
Db	2161	GTAACAAAGCAAAATGAAACAGACAGTAAGAAAGACATGACGTATCTTCCCAAGCTGA	2220
QY	2221	AGTTAAACAAATGCACTGCTGTTCTTTACTAAGTGTCAAATPAACGAGTAACTTAAAGAT	2280
Db	2221	AGTTAAACAAATGCACTGCTGTTCTTTACTAAGTGTCAAATPAACGAGTAACTTAAAGAT	2280
QY	2281	TTGTCAATCTTACGCTTCCAAAGAGAAAGAAAAAGAGAAAACGTAAAGTGT	2340
Db	2281	TTGTCAATCTTACGCTTCCAAAGAGAAAGAAAAAGAGAAAACGTAAAGTGT	2340
QY	2341	CTAATPAATGCTGAAGACCCCAAAAGATCTCATGTTAATGAGGAAAGGTTTGCAAACTG	2400
Db	2341	CTAATPAATGCTGAAGACCCCAAAAGATCTCATGTTAATGAGGAAAGGTTTGCAAACTG	2400
QY	2401	AAAGATCTGTAGAAGTGAAGATTTTACAGTGTAACCTGTAATGATGCACTCAG	2460
Db	2401	AAAGATCTGTAGAAGTGAAGATTTTACAGTGTAACCTGTAATGATGCACTCAG	2460
QY	2461	AAAGTATCTCTTACTGTGAAGTTAGCACTTAGGGAAGGCAAAAAACAGAACCAATTAAT	2520
Db	2461	AAAGTATCTCTTACTGTGAAGTTAGCACTTAGGGAAGGCAAAAAACAGAACCAATTAAT	2520
QY	2521	GTTGTAGTCAAGTGTGAGCATTTGAAAAACCCCAAGGACCTAATTCATGTTGTTCCAAAG	2580
Db	2521	GTTGTAGTCAAGTGTGAGCATTTGAAAAACCCCAAGGACCTAATTCATGTTGTTCCAAAG	2580
QY	2581	ATAATATGAATGACACAGAAAGGCTTAAGTATCCATGAGGACATGAAGTTAAACAAGTCTC	2640
Db	2581	ATAATATGAATGACACAGAAAGGCTTAAGTATCCATGAGGACATGAAGTTAAACAAGTCTC	2640
QY	2641	GGGAACCAAGCATTAGAAAAATGGAAGAAAGTGAACCTTATGCTCAGTATTTGCAAGATACAT	2700
Db	2641	GGGAACCAAGCATTAGAAAAATGGAAGAAAGTGAACCTTATGCTCAGTATTTGCAAGATACAT	2700
QY	2701	TCAAAGTTTCAAAAGCGCCAGTCATTTGCTCTGTTTCAAATTCAGGAATGCAAGAGG	2760
Db	2701	TCAAAGTTTCAAAAGCGCCAGTCATTTGCTCTGTTTCAAATTCAGGAATGCAAGAGG	2760
QY	2761	AATGTGCAACATTTCTGCCCCCTGCGGTCTTTAAAGAAACCAAGTCCAAAAGTCACTT	2820
Db	2761	AATGTGCAACATTTCTGCCCCCTGCGGTCTTTAAAGAAACCAAGTCCAAAAGTCACTT	2820
QY	2821	TTGAATGTGAACAAAAGGAAGAAATCAAGGAAAGAAATGAAGTCTAATATCAAGCTGTAC	2880
Db	2821	TTGAATGTGAACAAAAGGAAGAAATCAAGGAAAGAAATGAAGTCTAATATCAAGCTGTAC	2880
QY	2881	AGACGATTAAATATCACTGACGGCTTCTGTGTGTTGTCAGAAAGATTAAGCAATGATA	2940

Db	2881	AGACGTTAAATACATGCAAGGCTTTCTGTGGTGGTCAAGAAAGTAAGCAGTTATATA	2940
Oy	2941	ATGCGAAATAGTATCAAAAGAGGCTCTAGGTTTGTCTATCATCTCAGTTCAGAGCA	3000
Db	2941	ATGCCAAATGTAGTTCMAAGAGGCGCTGAGTTTGTCTATCATCTCAGTTCAGAGCA	3000
Oy	3001	ACGAAATCGACTCAATTACTCCAAATAAACATGAGACTTTTACAAACCATATCTGATAC	3060
Db	3001	ACGAAATCGACTCAATTACTCCAAATAAACATGAGACTTTTACAAACCATATCTGATAC	3060
Oy	3061	CACCACTTTTCCCATCAAGTCACTTTGTTAAACTTAATGTAAAGAAAATCTGTAGAGG	3120
Db	3061	CACCACTTTTCCCATCAAGTCACTTTGTTAAACTTAATGTAAAGAAAATCTGTAGAGG	3120
Oy	3121	AAAACCTTGAAGAACATTCATGTCCACCTGAAAGAAATGGGAAATGAGAACATTCGAA	3180
Db	3121	AAAACCTTGAAGAACATTCATGTCCACCTGAAAGAAATGGGAAATGAGAACATTCGAA	3180
Oy	3181	GTACAGTAGACAATTAAGCCGTAATAACATTAAGAAAAATGTTTTAAAGAGCCAGCT	3240
Db	3181	GTACAGTAGACAATTAAGCCGTAATAACATTAAGAAAAATGTTTTAAAGAGCCAGCT	3240
Oy	3241	CAAGCAATTTAATGAAGTAGTTCGAGTACTAATGAAGGGGCTCCAGATTTATGAAA	3300
Db	3241	CAAGCAATTTAATGAAGTAGTTCGAGTACTAATGAAGGGGCTCCAGATTTATGAAA	3300
Oy	3301	TAGGTTCCAGTATGAAAAATTCAAGCAGAACTAGGTAGAGAAACAGAGGGCCAAATTTGA	3360
Db	3301	TAGGTTCCAGTATGAAAAATTCAAGCAGAACTAGGTAGAGAAACAGAGGGCCAAATTTGA	3360
Oy	3361	ATGCTATGCTTAGATTAGGGGTTTTGCAACCTGAGGTCCTATAAACAAAGTCTTCGGAA	3420
Db	3361	ATGCTATGCTTAGATTAGGGGTTTTGCAACCTGAGGTCCTATAAACAAAGTCTTCGGAA	3420
Oy	3421	GTAATGTGAACATCTCTGAAATTAAGAAAGCAAGATATGAAGAGTAGTTCAGCTGTTA	3480
Db	3421	GTAATGTGAACATCTCTGAAATTAAGAAAGCAAGATATGAAGAGTAGTTCAGCTGTTA	3480
Oy	3481	ATACAGATTTCTCTCCATATCTGATTTCCAGATTACTTAGAACAGCCTATGGAAGTAGTC	3540
Db	3481	ATACAGATTTCTCTCCATATCTGATTTCCAGATTACTTAGAACAGCCTATGGAAGTAGTC	3540
Oy	3541	ATGCATCTCAGGTTTGTCTGAGACACCTGATGACCTGTATGATGATGTAATTAAGG	3600
Db	3541	ATGCATCTCAGGTTTGTCTGAGACACCTGATGACCTGTATGATGATGTAATTAAGG	3600
Oy	3601	AAGATACCTAGTTTGTCTGAAATATGACATTAAGAAAGTTCGTGCTTTTAAAGCAAAAGCG	3660
Db	3601	AAGATACCTAGTTTGTCTGAAATATGACATTAAGAAAGTTCGTGCTTTTAAAGCAAAAGCG	3660
Oy	3661	TCCAGAGAGAGAGGCTTACAGAGAGCTCCAGCCCTTTCAACCATACACATTTGGCTCAGG	3720
Db	3661	TCCAGAGAGAGAGGCTTACAGAGAGCTCCAGCCCTTTCAACCATACACATTTGGCTCAGG	3720
Oy	3721	GTTACCGAAGAGGGGCCAAAGAAATTAAGAGTCTCTAGAAAGAGAACTTATATGAGAGATG	3780
Db	3721	GTTACCGAAGAGGGGCCAAAGAAATTAAGAGTCTCTAGAAAGAGAACTTATATGAGAGATG	3780
Oy	3781	AAGAGCTTCCTGCTTCCAAACACTTGTATTTGGTAAAGTAAACAATATACCTTCAGT	3840
Db	3781	AAGAGCTTCCTGCTTCCAAACACTTGTATTTGGTAAAGTAAACAATATACCTTCAGT	3840
Oy	3841	CTACTAGGCAATGACACCGTGTCTACCGAGTGTCTGCTAAGAACACAGAGAGAAATTAAT	3900
Db	3841	CTACTAGGCAATGACACCGTGTCTACCGAGTGTCTGCTAAGAACACAGAGAGAAATTAAT	3900
Oy	3901	TATCATTTGAAGAAATAGCTTAATATGACTGCAATTAACAGGTAAATTTGGCAAAAGCATCTC	3960
Db	3901	TATCATTTGAAGAAATAGCTTAATATGACTGCAATTAACAGGTAAATTTGGCAAAAGCATCTC	3960
Oy	3961	AGGAACATCACCTTAGTAGAGAAACAAATGTTCTGACTGTTTCTTACACGTGCA	4020
Db	3961	AGGAACATCACCTTAGTAGAGAAACAAATGTTCTGACTGTTTCTTACACGTGCA	4020

Db 3961 AGGAACATCACCCTTAGTAGAGAAACAAATGTTCTGCTAGCTTTTCTTCACAGTGCA 4020  
 Qy 4021 GTGAATGGAAGACTTGACTGCAAAATACAAACACCCAGGATCCTTTCTTGATGGTCTT 4080  
 Db 4021 GTGAATGGAAGACTTGACTGCAAAATACAAACACCCAGGATCCTTTCTTGATGGTCTT 4080  
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 Qy 4141 TTTTCAGATGATGAAAGAAAGAGACGGGCTTGAAAGAAATATATCAAGAGGCAAGCA 4200  
 Db 4141 TTTTCAGATGATGAAAGAAAGAGACGGGCTTGAAAGAAATATATCAAGAGGCAAGCA 4200  
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 Db 4321 AACATACCTGATTAAGCTCCAGCAGAAATGGCTGAATAGAGCTGTGTTGAACACG 4380  
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 Qy 4681 ACTACCCATCTCAAGAGAGCTCTTAAGGTTGTTGATGATGATGATGATGATGATGATG 4740  
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 Qy 4741 AGTCTGGGCGCACAGATTTGAGGAAACATCTTACTTGGCAAGGCAAGATCTTGAAGGAA 4800  
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 Qy 4801 CCCCTTACCTGGAATCTGGAATCAGGCTCTTCTGATGAGACCTGAATCTGATCTCTG 4860  
 Db 4801 CCCCTTACCTGGAATCTGGAATCAGGCTCTTCTGATGAGACCTGAATCTGATCTCTG 4860  
 Qy 4861 AAGACAGAGCCCGCAGAGTCAAGCTCGTGTGGCAATACCATCTTCAACCTCTGATGTA 4920  
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 Db 4921 AAGTTCCTCAATTTGAAAGTTGCAATCTGCCAGAGGTCAGCTGCTGCTACTACTG 4980  
 Qy 4981 ATACTGCTGGGTATTAATGCAATGAAAGAGTGTGAGCAGGAGGAGGAGGAGGAGGAGG 5040  
 Db 4981 ATACTGCTGGGTATTAATGCAATGAAAGAGTGTGAGCAGGAGGAGGAGGAGGAGGAGG 5040  
 Qy 5041 CTTCAACAGAAAGGCTCAACAAAGATGTCCATGATGTGTGTGTGTGTGTGTGTGTGTGT 5100  
 Db 5041 CTTCAACAGAAAGGCTCAACAAAGATGTCCATGATGTGTGTGTGTGTGTGTGTGTGTGT 5100

Qy 5101 AATTATGCTGCTGTGATCAAGTTTGGCAGAAAAACACACATCATTTAATCTAATTA 5160  
 Db 5101 AATTATGCTGCTGTGATCAAGTTTGGCAGAAAAACACACATCATTTAATCTAATTA 5160  
 Qy 5161 CTGAAGAGACTACTCATGTTGTTATGAAGAACAGATGCTGAGTTGTGTGAGACGAC 5220  
 Db 5161 CTGAAGAGACTACTCATGTTGTTATGAAGAACAGATGCTGAGTTGTGTGAGACGAC 5220  
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 Db 5221 TGAATATTTTCTAGAAATTCGCGAGGAGAAATGGGTAGTATGATTTTCTGGGTGACCC 5280  
 Qy 5281 AGCTATTAAGAAAGAAATATGCTGAATGAGCATGATTTTGAAGTCTAGAGAGATGTGG 5340  
 Db 5281 AGCTATTAAGAAAGAAATATGCTGAATGAGCATGATTTTGAAGTCTAGAGAGATGTGG 5340  
 Qy 5341 TCAATGAAAGAAACCAAGGTCCTCAAGCGAGAGAAATCCAGAGACAGAAAGATCT 5400  
 Db 5341 TCAATGAAAGAAACCAAGGTCCTCAAGCGAGAGAAATCCAGAGACAGAAAGATCT 5400  
 Qy 5401 TCAAGGGGCTAGAAATCTGTTGCTATGAGGCTTCAACATGCTCCACATCACTGG 5460  
 Db 5401 TCAAGGGGCTAGAAATCTGTTGCTATGAGGCTTCAACATGCTCCACATCACTGG 5460  
 Qy 5461 AATGATGATACAGCTGT 5520  
 Db 5461 AATGATGATACAGCTGT 5520  
 Qy 5521 GCACAGGTGTCCACCAATGTTGTTGTGACAGCCAGATGCTGACAGAGCAATGAGT 5580  
 Db 5521 GCACAGGTGTCCACCAATGTTGTTGTGACAGCCAGATGCTGACAGAGCAATGAGT 5580  
 Qy 5581 TCCATGCAATTTGGGCAATGT 5640  
 Db 5581 TCCATGCAATTTGGGCAATGT 5640  
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 Db 5641 GTGTAGCACTTACAGAGGCGAGGCTGAGACCTACTGATCCAGATCCGCCACA 5700  
 Qy 5701 GCCACTACTGA 5711  
 Db 5701 GCCACTACTGA 5711

RESULT 7  
 US-09-074-476-3  
 ; Sequence 3, Application US/09074476  
 ; Patent No. 6130322  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Murphy, Patricia D.  
 ; APPLICANT: Allen, Antonette C.  
 ; APPLICANT: Alvares, Christopher P.  
 ; APPLICANT: Clitz, Brenda S.  
 ; APPLICANT: Olson, Sheri J.  
 ; APPLICANT: Thudner, Denise  
 ; APPLICANT: Zeng, Bin  
 ; TITLE OF INVENTION: Coding Sequences of the Human  
 ; TITLE OF INVENTION: BRCA1 Gene  
 ; NUMBER OF SEQUENCES: 72  
 ; CORRESPONDENCE ADDRESS:  
 ; ADDRESSEE: Howrey & Simon  
 ; STREET: 1299 Pennsylvania Avenue N. W.  
 ; CITY: Washington  
 ; STATE: DC  
 ; COUNTRY: USA  
 ; ZIP: 20004  
 ; COMPUTER READABLE FORM:  
 ; MEDIUM TYPE: Floppy disk  
 ; COMPUTER: IBM PC compatible  
 ; OPERATING SYSTEM: PC-DOS/MS-DOS  
 ; SOFTWARE: PatentIn Release #1.0, Version #1.30

CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/074,476  
FILING DATE:  
CLASSIFICATION:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 09/074,453  
FILING DATE:  
ATTORNEY/AGENT INFORMATION:  
NAME: Albert P. Halluin  
REGISTRATION NUMBER: 25,227  
REFERENCE/DOCKET NUMBER: 5371.34.US01  
TELEPHONE: 650-463-8109  
TELEFAX: 650-463-8109  
INFORMATION FOR SEQ ID NO: 3:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 5711 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: not relevant  
TOPOLOGY: linear  
MOLECULE TYPE: cDNA  
ORIGINAL SOURCE:  
ORGANISM: Homo sapiens  
STRAIN: BRCA1 (om12)  
POSITION IN GENOME:  
CHROMOSOME/SEGMENT: 17  
MAP POSITION: 17q21  
US-09-074-476-3

Query Match 100.0%; Score 5709.4; DB 3; Length 5711;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 5710; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 AGCTGGCTGAGACTTCTCTGAGACCCCGCACAGGCTGTGGGTTTCTGATTAACCTGGCC 60  
DB 1 AGCTGGCTGAGACTTCTCTGAGACCCCGCACAGGCTGTGGGTTTCTGATTAACCTGGCC 60  
QY 61 CTTGGGCTCAGAGGCTTCAACCTCTGCTGGGTTAAAGTTCATTGGAAGAAAGAA 120  
DB 61 CTTGGGCTCAGAGGCTTCAACCTCTGCTGGGTTAAAGTTCATTGGAAGAAAGAA 120  
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DB 121 TGGATTATCTGCTCTTCCGCTTGAAGAGTACAAATGTCTAATATGCTATGACAGAAA 180  
QY 121 TGGATTATCTGCTCTTCCGCTTGAAGAGTACAAATGTCTAATATGCTATGACAGAAA 180  
DB 121 TGGATTATCTGCTCTTCCGCTTGAAGAGTACAAATGTCTAATATGCTATGACAGAAA 180  
QY 181 TCTTGAAGTCCCATCTGTCTGAGGTTGATCAAGAACTGTCTCCCAAAAGTGTGACC 240  
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DB 241 ACATATTTTGCAGAAATTTTGCAGTGAAGAACTTCAACGAGAAAGAGGCTTCAAGT 300  
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DB 301 GTCTTTATATGAAGATGATATACCAAAAGAGGCTTCAAGAAAGTACGAGATTAGTC 360  
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DB 361 AACTTGTGAAGAGCTATTTGAATCATTTTGTCTTTTCAAGTTACAGAGTTTGGAGT 420  
QY 421 ATGCAACAGCTATATTTTGCAGAAAGAAAGAAATTAATCTCTCAACATCTAAAGATG 480  
DB 421 ATGCAACAGCTATATTTTGCAGAAAGAAAGAAATTAATCTCTCAACATCTAAAGATG 480  
QY 481 AAGTTTATCATCCAAAGATGGGCTACAGAAACCGTCCCAAAAGACTTCTACAGAGT 540  
DB 481 AAGTTTATCATCCAAAGATGGGCTACAGAAACCGTCCCAAAAGACTTCTACAGAGT 540  
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QY 541 AACCCGAAATCTTCTTGGCAGAAACCAAGTCTCAAGTCTCAACTCTCTTAACTTTGAA 600  
DB 541 AACCCGAAATCTTCTTGGCAGAAACCAAGTCTCAAGTCTCAACTCTCTTAACTTTGAA 600

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QY 661 AATTGGGATCTGATTTCTTGAAGATACCGTTAATAGGCACTTATTTGCAAGTGGAG 720  
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QY 721 ATCAAGAAATTTGTCAAATCAACCTCCCAAGGAAACGAGGATGAATCACTTTGATTTG 780  
DB 721 ATCAAGAAATTTGTCAAATCAACCTCCCAAGGAAACGAGGATGAATCACTTTGATTTG 780  
QY 781 CAAAAAGGCTGCTTGTGAATTTTCTGAGACGATGTAACTAAATCTGAATCATCTAAC 840  
DB 781 CAAAAAGGCTGCTTGTGAATTTTCTGAGACGATGTAACTAAATCTGAATCATCTAAC 840  
QY 841 CCAGTAATATGATTTGAAACCACTGAGAGCGTGACGTTGAGAGGATCCAGAAAAGT 900  
DB 841 CCAGTAATATGATTTGAAACCACTGAGAGCGTGACGTTGAGAGGATCCAGAAAAGT 900  
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DB 901 ATTCAGGATGTTCTGTTTCAAACTTTCATGAGAGGCACTGAGCAAAATCTCATGCGCA 960  
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DB 961 GCTCATTTACACATGAGAAACGAGATTATTAATCTCACTAAAGACAGATGATGAGAAA 1020  
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QY 1261 AAGTTAATGAGTGTTCAGAGAGTGAATGATGAGTGTGATGATCACTCAATGATG 1320  
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QY 1321 GGGAGTCTGAATCAAAATGCCAAAGTGAATGATGATGATGATGATGATGATGATG 1380  
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DB 1381 AATATTTCTGTTTCTTCAAGAAATTAATGATGATGATGATGATGATGATGATGATG 1440  
QY 1441 TATGTAAGTGAAGAGATGATGATGATGATGATGATGATGATGATGATGATGATG 1500  
DB 1441 TATGTAAGTGAAGAGATGATGATGATGATGATGATGATGATGATGATGATGATG 1500  
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DB 1501 TTGGGAAACCTATCTGAGAAAGGCAAGCTCCCAATCTTAAGCATTAATCTGAAAATC 1560  
QY 1561 TAAATTAAGAGCAATTTGTTAATGAGCAAGATTAATCAAGAGGTCCTTCAAAATA 1620  
DB 1561 TAAATTAAGAGCAATTTGTTAATGAGCAAGATTAATCAAGAGGTCCTTCAAAATA 1620  
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DB 1621 AATTAAGCGTAAAGAGAGCACTTACATGAGGCTTCACTGAGGATTTTATCAAGAAAG 1680  
QY 1681 CAGATTTGGAGTTCAAAAGACTCTGTGAATGATTAATCAAGGAACTAACCAAGGAGC 1740



Db 1681 CAAATTTGGAGTTCAAAAGCTCTCTGAAATGATTAATTCAGGGAGCTAACAAACGAGC 1740  
Qy 1741 AGATGTCAGATGATGATATTTACTAATGTGTCATGGAATTAACAAAGGTGATT 1800  
Db 1741 AGAATGTCAGATGATATTTACTAATGTGTCATGGAATTAACAAAGGTGATT 1800  
Qy 1801 CTATTCAGAAATGAGAAAATCTTAACCAATAGATCACTCGAATAAAGAAATCTGCTTCA 1860  
Db 1801 CTATTCAGAAATGAGAAAATCTTAACCAATAGATCACTCGAATAAAGAAATCTGCTTCA 1860  
Qy 1861 AAACGAAAGCTGAACCTTAATAGCAGAGTATAGCAATATGAACTCGAAATTAATATCC 1920  
Db 1861 AAACGAAAGCTGAACCTTAATAGCAGAGTATAGCAATATGAACTCGAAATTAATATCC 1920  
Qy 1921 ACAATTCAAAGACCTTAAGAAATAGCTGAGAGAGAAATCTTCAACAGGATATTC 1980  
Db 1921 ACAATTCAAAGACCTTAAGAAATAGCTGAGAGAGAAATCTTCAACAGGATATTC 1980  
Qy 1981 ATGCGCTTGAATAGTATGATGATGAATCTAAGCCCACTAATTTGATGAAATTCGAAA 2040  
Db 1981 ATGCGCTTGAATAGTATGATGATGAATCTAAGCCCACTAATTTGATGAAATTCGAAA 2040  
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Db 2041 TTGATAGTTGTTCTAGCAGTGAAGATTAAGAAAAGTAAACAAATGCAATGCA 2100  
Qy 2101 GGCACAGCAGAAAACCTTAACCTCACTGAGATTAAGAACTGCACTGAGCCCAAGAA 2160  
Db 2101 GGCACAGCAGAAAACCTTAACCTCACTGAGATTAAGAACTGCACTGAGCCCAAGAA 2160  
Qy 2161 GTAAACAAGCCAAATGAACAGATTAAGAAAGATGACATGATTAATCTTCCAGAGCTGA 2220  
Db 2161 GTAAACAAGCCAAATGAACAGATTAAGAAAGATGACATGATTAATCTTCCAGAGCTGA 2220  
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Db 2221 AGTTAAACAAATGACCTGTTCTTTTCTAATGTTCAATATACCAATGAACTTAAGAAAT 2280  
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RESULT 8  
 US-08-798-691-3  
 Patent No. 5750400  
 Sequence 3, Application US/08798691  
 GENERAL INFORMATION:  
 APPLICANT: Murphy, Patricia D.  
 APPLICANT: Allen, Antoinette C.  
 APPLICANT: Alvarez, Christopher P.  
 APPLICANT: Critz, Brenda S.  
 APPLICANT: Olson, Sheri J.  
 APPLICANT: Schelter, Denise B.  
 APPLICANT: Zeng, Bin  
 TITLE OF INVENTION: Coding Sequences of the Human  
 TITLE OF INVENTION: BRCA1 Gene  
 NUMBER OF SEQUENCES: 72  
 CORRESPONDENCE ADDRESS:  
 ADDRESSEE: ONCORMED  
 STREET: 200 Perry Parkway  
 CITY: Gaithersburg  
 STATE: MD

COUNTRY: USA  
 ZIP: 20877  
 COMPUTER READABLE FORM:  
 MEDIUM TYPE: Floppy disk  
 COMPUTER: IBM PC compatible  
 OPERATING SYSTEM: PC-DOS/MS-DOS  
 SOFTWARE: PatentIn Release #1.0, Version #1.30  
 CURRENT APPLICATION DATA:  
 APPLICATION NUMBER: US/08/798,691  
 FILING DATE: 12-Feb-97  
 CLASSIFICATION: 435  
 ATTORNEY/AGENT INFORMATION:  
 NAME: Thomas Galligos  
 REGISTRATION NUMBER: 32,692  
 REFERENCE/DOCKET NUMBER: PA-0054CIP  
 TELECOMMUNICATION INFORMATION:  
 TELEPHONE: 301-527-2051  
 TELEFAX: 301-208-6997  
 INFORMATION FOR SEQ ID NO: 3:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 5711 base pairs  
 TYPE: nucleic acid  
 STRANDEDNESS: not relevant  
 TOPOLOGY: linear  
 MOLECULE TYPE: cDNA  
 ORIGINAL SOURCE:  
 ORGANISM: Homo sapiens  
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 POSITION IN GENOME:  
 CHROMOSOME/SEGMENT: 17  
 MAP POSITION: 17q21  
 US-08-798-691-3

Query Match 99.8%; Score 5701.4; DB 1; Length 5711;  
 Best Local Similarity 99.9%; Pred. No. 0;  
 Matches 5705; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

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RESULT 9  
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 ; Sequence 3, Application us/08825487A  
 ; Patent No. 6048689  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Murphy, Patricia D.  
 ; APPLICANT: White, Margie B.  
 ; TITLE OF INVENTION: METHODS FOR IDENTIFYING VARIATIONS IN POLYNUCLEOTIDE SEQUENCE  
 ; NUMBER OF SEQUENCES: 110  
 ; CORRESPONDENCE ADDRESS:  
 ; ADDRESS: Howrey & Simon  
 ; STREET: 1299 Pennsylvania Avenue., N.W.  
 ; CITY: Washington,  
 ; STATE: DC  
 ; COUNTRY: USA  
 ; ZIP: 20004





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RESULT 10  
US-09-074-476-5  
; Sequence 5, Application US/09074476  
; Patent No. 6130322  
; GENERAL INFORMATION:  
; APPLICANT: Murphy, Patricia D.  
; APPLICANT: Allen, Antonette C.  
; APPLICANT: Alvarez, Christopher P.  
; APPLICANT: Critz, Brenda S.  
; APPLICANT: Olson, Sheri J.  
; APPLICANT: Thurber, Denise  
; APPLICANT: Zeng, Bin  
; TITLE OF INVENTION: Coding Sequences of the Human  
; TITLE OF INVENTION: BRCA1 Gene

	CORRESPONDENCE ADDRESS:	72
	ADDRESSEE: Howrey & Simon	
	STREET: 1299 Pennsylvania Avenue N. W.	
	CITY: Washington	
	STATE: DC	
	COUNTRY: USA	
	ZIP: 20004	
	COMPUTER READABLE FORM:	
	MEDIUM TYPE: Floppy disk	
	OPERATING SYSTEM: IBM PC compatible	
	SOFTWARE: Patent In Release #1.0, Version #1.30	
	CURRENT APPLICATION DATA:	
	APPLICATION NUMBER: US/09/074,476	
	FILING DATE:	
	CLASSIFICATION:	
	PRIOR APPLICATION DATA:	
	APPLICATION NUMBER: 09/074,453	
	FILING DATE:	
	ATTORNEY/AGENT INFORMATION:	
	NAME: Albert P. Halluin	
	REGISTRATION NUMBER: 25,227	
	REFERENCE/DOCKET NUMBER: 5371.34.US01	
	TELECOMMUNICATION INFORMATION:	
	TELEPHONE: 650-463-8109	
	TELEFAX: 650-463-8400	
	INFORMATION FOR SEQ ID NO: 5:	
	SEQUENCE CHARACTERISTICS:	
	LENGTH: 5711 base pairs	
	TYPED: nucleic acid	
	STRANDEDNESS: not relevant	
	TOPOLOGY: linear	
	MOLECULE TYPE: cDNA	
	ORGANISM SOURCE:	
	ORGANISM: Homo sapiens	
	STRAIN: BRCA1 (oml3)	
	POSITION IN GENOME:	
	CHROMOSOME/SEGMENT: 17	
	MAP POSITION: 17q21	
	/	
	US-09-074-476-5	
	Query Match	99.8%; Score 5701.4; DB 3; Length 5711;
	Best Local Similarity	99.9%; Pred. No. 0;
	Matches 5705; Conservative	0; Mismatches 6; Indels 0; Gaps 0;
OY	AGCTGCGTGAACCTTCGTGGACCAGCCGCCATTTGCAGATACTGGGCC	60
Dd	1 AGCTGCGTGAACCTTCGTGGACCAGCCGCCATTTGCAGATACTGGGCC	60
OY	61 COTGGCCTCAGAAGGACTTGACAACCTCTGCTGGTAAGTTCAATTGAAACAAAAGAA	120
Dd	61 COTGGCCTCAGAAGGACTTGACAACCTCTGCTGGTAAGTTCAATTGAAACAAAAGAA	120
OY	121 TGAATTAATCTGCTCTTGCGGTTAAGAACATCAAAATGCTCATTAATGCTATGCAGAAAA	180
Dd	121 TGAATTAATCTGCTCTTGCGGTTAAGAACATCAAAATGCTCATTAATGCTATGCAGAAAA	180
OY	181 TGATTAAGTAGTCCCCTGCTGGAGTTGATCAAGAACCTGTCCTCCAAGTAGTGACC	240
Dd	181 TGATTAAGTAGTCCCCTGCTGGAGTTGATCAAGAACCTGTCCTCCAAGTAGTGACC	240
OY	241 ACATATTTTGGCAAATTTTGGCAATGCTGAAACCTTCAACAGAAAGAGGACTTCAAGT	300
Dd	241 ACATATTTTGGCAAATTTTGGCAATGCTGAAACCTTCAACAGAAAGAGGACTTCAAGT	300
OY	301 GTCTCTTAATGTAAGATGATATTAACCAAAAGAGGACTTCAAGAAAGTACGAGATTTAGTC	360
Dd	301 GTCTCTTAATGTAAGATGATATTAACCAAAAGAGGACTTCAAGAAAGTACGAGATTTAGTC	360
OY	361 AACTGTGTAAGAGCTATTTGAAATCATTTGGCTTTTCAGCTTACACAGATTTGGAGT	420
Dd	361 AACTGTGTAAGAGCTATTTGAAATCATTTGGCTTTTCAGCTTACACAGATTTGGAGT	420
OY	420 AACCTGTTGAAGAGCTATTTGAAATCATTTGGCTTTTCAGCTTACACAGATTTGGAGT	420
Dd	420 AACCTGTTGAAGAGCTATTTGAAATCATTTGGCTTTTCAGCTTACACAGATTTGGAGT	420

OY	421	ATGCAACAGCTATATATTTGGCAAAAAAGAAAATACCTCCCGAACAATCTAAAAGT	480
Db	421	ATGCAACAGCTATATATTTGGCAAAAAAGAAAATACCTCCCGAACAATCTAAAAGT	480
OY	481	AAGTTTCTATCATCCAAAGTATGGGCTACAGAAACCGTGCCAAAAGACTTTCAGAGTG	540
Db	481	AAGTTTCTATCATCCAAAGTATGGGCTACAGAAACCGTGCCAAAAGACTTTCAGAGTG	540
OY	541	AAACCGAAAATCTCTTCTTGCAAGAAACAGTCTCAGTGTCCAACTCTTAACTTGGAA	600
Db	541	AAACCGAAAATCTCTTCTTGCAAGAAACAGTCTCAGTGTCCAACTCTTAACTTGGAA	600
OY	601	CTGTGAGAACTCTAGGACAAAGAGGGGATACAAACCTCAAAAGACGTCTGTACATTTG	660
Db	601	CTGTGAGAACTCTAGGACAAAGAGGGGATACAAACCTCAAAAGACGTCTGTACATTTG	660
OY	661	AATTGGATCTGATTCCTTGGAAGATACCGTTTAAAGCACTTATTTGCAGTGTGGAG	720
Db	661	AATTGGATCTGATTCCTTGGAAGATACCGTTTAAAGCACTTATTTGCAGTGTGGAG	720
OY	721	ATCAAGATTTGTACAAATCACCCCTCAAGAACCGGATGAAATCAGTTTGGATTCTG	780
Db	721	ATCAAGATTTGTACAAATCACCCCTCAAGAACCGGATGAAATCAGTTTGGATTCTG	780
OY	781	CAAAAAAGGCGCTTGGAATTTTCTGAGAGGATGTACAAATATCTGAATCATCATAC	840
Db	781	CAAAAAAGGCGCTTGGAATTTTCTGAGAGGATGTACAAATATCTGAATCATCATAC	840
OY	841	CCAGTAATATATGATTTGAAACCACTGAGAAAGCGTGACGTGAGAGGATCCAGAAAAGT	900
Db	841	CCAGTAATATATGATTTGAAACCACTGAGAAAGCGTGACGTGAGAGGATCCAGAAAAGT	900
OY	901	ATCAGGGTATGTTCTGTTTCAAACCTTGCAATGTGAGGCCATGTGGCAAAATCTCATGGCA	960
Db	901	ATCAGGGTATGTTCTGTTTCAAACCTTGCAATGTGAGGCCATGTGGCAAAATCTCATGGCA	960
OY	961	GCTCATTTACACATGAGAAACAGCAGTTTATTAATCACTTAAAGACAGATGTAGTGAATA	1020
Db	961	GCTCATTTACACATGAGAAACAGCAGTTTATTAATCACTTAAAGACAGATGTAGTGAATA	1020
OY	1021	AGCGTGAATTTGTATATTAAGCAAAACGCTGGCTTAGCAAGAGGCCAATTAACAGAT	1080
Db	1021	AGCGTGAATTTGTATATTAAGCAAAACGCTGGCTTAGCAAGAGGCCAATTAACAGAT	1080
OY	1081	GGGCTGGAAGTAAGAAACATGTATATGATAGCCGACCTCCACGACAGAAAAAAGGTAG	1140
Db	1081	GGGCTGGAAGTAAGAAACATGTATATGATAGCCGACCTCCACGACAGAAAAAAGGTAG	1140
OY	1141	ATCTGAATGCTGATCCCTGTGTAGAGAAAGAAATGGAATTAACAGAACTGCGCATCT	1200
Db	1141	ATCTGAATGCTGATCCCTGTGTAGAGAAAGAAATGGAATTAACAGAACTGCGCATCT	1200
OY	1201	CAGAGAAATCTAGAGATCTGAAATATGTTCTTGGAATTAACACTTAAATGACAGACTTCAGA	1260
Db	1201	CAGAGAAATCTAGAGATCTGAAATATGTTCTTGGAATTAACACTTAAATGACAGACTTCAGA	1260
OY	1261	AAGTTAATAGATGTTTTCCAGAAAGTATGAACTGTAAGTTCTGATGATCTCAACATGATG	1320
Db	1261	AAGTTAATAGATGTTTTCCAGAAAGTATGAACTGTAAGTTCTGATGATCTCAACATGATG	1320
OY	1321	GGGAGTCTGAATCAAAATGCCAAAGTAGCGTGTATTTGGAAGTTTCTTAAATGAGGTAGATG	1380
Db	1321	GGGAGTCTGAATCAAAATGCCAAAGTAGCGTGTATTTGGAAGTTTCTTAAATGAGGTAGATG	1380
OY	1381	AATATTTCTGTTCTTCAGAGAAAATAGACTTACGTGGCCAGTGATCTCATAGAGGCTTTTAA	1440
Db	1381	AATATTTCTGTTCTTCAGAGAAAATAGACTTACGTGGCCAGTGATCTCATAGAGGCTTTTAA	1440
OY	1441	TATGTAAAGTGAAGAGTTCACTCCAAATCAGTAGAGAGTAATATTGAACAATAATAT	1500
Db	1441	TATGTAAAGTGAAGAGTTCACTCCAAATCAGTAGAGAGTAATATTGAACAATAATAT	1500

QY	1501	TTGGGAAACTATCGGAAGAGGCAAGCTCCCACTTAAGCATGTAACTGAAATC	1560
Db	1501	TTGGGAAAGCTATCGGAAGAGGCAAGCTCCCACTTAAGCATGTAACTGAAATC	1560
QY	1561	TAAATATAGGAGCATTTGTTACTGAGCCACAGATTAATCAAGAGGCGTCCCTCAATA	1620
Db	1561	TAAATATAGGAGCATTTGTTACTGAGCCACAGATTAATCAAGAGGCGTCCCTCAATA	1620
QY	1621	AATTAAAGCTAAAGAGAGACTACATCAGGCTTCATCTGAGATTTTATCAAGAA	1680
Db	1621	AATTAAAGCTAAAGAGAGACTACATCAGGCTTCATCTGAGATTTTATCAAGAA	1680
QY	1661	CAGATTTGGCAGCTTAAAAAGACTCTGAAATGATTAATCAGGAACTTAACAAACGAGC	1740
Db	1661	CAGATTTGGCAGCTTAAAAAGACTCTGAAATGATTAATCAGGAACTTAACAAACGAGC	1740
QY	1741	AGAATGCTCAAGTGTATGATATTAATTAATAGTGGCATGAGAAATPAACAAAGGTGAT	1800
Db	1741	AGAATGCTCAAGTGTATGATATTAATTAATAGTGGCATGAGAAATPAACAAAGGTGAT	1800
QY	1801	CTATTCAGATGAGAAAAATCTTAACCCAAATGATCACTCGAAAAAGAAATCTGTTTCA	1860
Db	1801	CTATTCAGATGAGAAAAATCTTAACCCAAATGATCACTCGAAAAAGAAATCTGTTTCA	1860
QY	1861	AAACGAAGCTGCAACTTAAGCAGCAGTATAGCAATATGGAAGTCSAATTAATATCC	1920
Db	1861	AAACGAAGCTGCAACTTAAGCAGCAGTATAGCAATATGGAAGTCSAATTAATATATCC	1920
QY	1921	ACAAATTCAAAAGCAGCTTAATAAGATATAGCTGAGAGGAAGTCTTAACGAGGATATTC	1980
Db	1921	ACAAATTCAAAAGCAGCTTAATAAGATATAGCTGAGAGGAAGTCTTAACGAGGATATTC	1980
QY	1981	ATGCGCTTGAAGCTAGTAGTCAGTAGAAATCTTAAGCCCACTAATTTGATCTGAATTCGAAA	2040
Db	1981	ATGCGCTTGAAGCTAGTAGTCAGTAGAAATCTTAAGCCCACTAATTTGATCTGAATTCGAAA	2040
QY	2041	TTGATATGTTGTTCTTACGAGTGAAGATTAAGAAAAAAGTACACCAATTCGCACTCA	2100
Db	2041	TTGATATGTTGTTCTTACGAGTGAAGATTAAGAAAAAAGTACACCAATTCGCACTCA	2100
QY	2101	GGCAGAGCAAAAGCTTACAACATCAGTAAGGTTAAAGAACTGGCAACTGGACCAAGAA	2160
Db	2101	GGCAGAGCAAAAGCTTACAACATCAGTAAGGTTAAAGAACTGGCAACTGGACCAAGAA	2160
QY	2161	GTTAACAGGCCAAATGAAAGACAGACAAATTAAGACATGACAGAGTACTTTCCAGAGCTGA	2220
Db	2161	GTTAACAGGCCAAATGAAAGACAGACAAATTAAGACATGACAGAGTACTTTCCAGAGCTGA	2220
QY	2221	AGTTAACAAATGCACTGCTGTTCTTTTACTTAAGTGTCAAAATACAGTAAAGAAAT	2280
Db	2221	AGTTAACAAATGCACTGCTGTTCTTTTACTTAAGTGTCAAAATACAGTAAAGAAAT	2280
QY	2281	TTGTCAATCTTAGCCTTCCAGAGAAAGAAAAAGAGAAATCTGAAACAGTTAAAGTGT	2340
Db	2281	TTGTCAATCTTAGCCTTCCAGAGAAAGAAAAAGAGAAATCTGAAACAGTTAAAGTGT	2340
QY	2341	CTAATATATGCTGAAGACCCCAAGACTCATGTTTAAGTGAAGAAAGGTTTTGGCAAATG	2400
Db	2341	CTAATATATGCTGAAGACCCCAAGACTCATGTTTAAGTGAAGAAAGGTTTTGGCAAATG	2400
QY	2401	AAAGATCTGTAGAGTAGACAGTATTTCACTGTATCTGTATCTGATTTATGCACTCAGG	2460
Db	2401	AAAGATCTGTAGAGTAGACAGTATTTCACTGTATCTGTATCTGATTTATGCACTCAGG	2460
QY	2461	AAAGATCTCTTACTTCTGGAAGTTAGCACTCTTAGGAAAGCAAAAACAACCAATAAT	2520
Db	2461	AAAGATCTCTTACTTCTGGAAGTTAGCACTCTTAGGAAAGCAAAAACAACCAATAAT	2520
QY	2521	GTGTAGTCAGTGTGACAGATTGTAAGAAACCCCAAGGACTAATTCATGTGTTTCCAAAG	2580
Db	2521	GTGTAGTCAGTGTGACAGATTGTAAGAAACCCCAAGGACTAATTCATGTGTTTCCAAAG	2580
QY	2581	ATTAATAGAAATGACACAGAAAGCTTTAAATATCAATTGGGACATGAAATTAAACAAGTCT	2640

Db	2581	ATATATGAAATGACAACGAGAGCTTTAAGTATCCATTGGGACATGAAATTACCAAGTCC	2640
QY	2641	GGGAAACAGAGATAGAAATGGAGAAAGTGAATGTGACTCAGTATTTTGCAGAAATCAT	2700
Db	2641	GGGAAACAGAGATAGAAATGGAGAAAGTGAATGTGATGCTCAGTATTTTGCAGAAATCAT	2700
QY	2701	TCGAAGTTTCAAGGCGCAGTCAATTGGCTGTGTTTCAATCCAGAAATGCAGAGAGG	2760
Db	2701	TCAAGTTTCAAAACGCGCAGTCAATTGGCTGTGTTTCAAAATCCAGAAATGCAGAGAGG	2760
QY	2761	AATGCGAAGCTTCTGCGCCACTCTGGGTCCTTAAAGAAACAAAGTCCAAAGTCCACTT	2820
Db	2761	AATGCGAAGCTTCTCTGCCACTCTGGGTCCTTAAAGAAACAAAGTCCAAAGTCCACTT	2820
QY	2821	TTGGAATGGAACAAAAGGAGAAAATCAGGAAAAGATGAGTCTTATATCAAGCTGTAC	2880
Db	2821	TTGGAATGGAACAAAAGGAGAAAATCAGGAAAAGATGAGTCTTATATCAAGCTGTAC	2880
QY	2881	AGACAGTTAATATCACTGCAAGGCTTTCTGTGTTGGTCAAGAAATPAGCCAGTTGATA	2940
Db	2881	AGACAGTTAATATCACTGCAAGGCTTTCTGTGTTGGTCAAGAAATPAGCCAGTTGATA	2940
QY	2941	ATGCGAAATGTAGATCAAAAGAGGCTCTAGGTTTGTCTATCATCTCAGTTCAGAGGCA	3000
Db	2941	ATGCGAAATGTAGATCAAAAGAGGCTCTAGGTTTGTCTATCATCTCAGTTCAGAGGCA	3000
QY	3001	ACGAAATCGAGCTCATTTCTCCAAATPAAACATGACCTTTTCAAAACCCATATGCTATAC	3060
Db	3001	ACGAAATCGAGCTCATTTCTCCAAATPAAACATGACCTTTTCAAAACCCATATGCTATAC	3060
QY	3061	CACCACTTTTCCATCAAGTCAATTGTTTAAACCTAAATGTAGAAAATCTGCTAGAGG	3120
Db	3061	CACCACTTTTCCATCAAGTCAATTGTTTAAACCTAAATGTAGAAAATCTGCTAGAGG	3120
QY	3121	AAAATTGTAGAGAACATTCATATGTCACCTGAAACAGAAATGGGAAATGAGAACATTCGCA	3180
Db	3121	AAAATTGTAGAGAACATTCATATGTCACCTGAAACAGAAATGGGAAATGAGAACATTCGCA	3180
QY	3181	GTACAGTGAAGACATTAATGACCGTATATACTTAGAGAAAATGTTTTTAAAGAGCCAGCT	3240
Db	3181	GTACAGTGAAGACATTAATGACCGTATATACTTAGAGAAAATGTTTTTAAAGAGCCAGCT	3240
QY	3241	CAAGCAATATTTAATGAAGTAGGTTCCAGTACTAATGAAGTGCGGCTCCAGTATTAATGAA	3300
Db	3241	CAAGCAATATTTAATGAAGTAGGTTCCAGTACTAATGAAGTGCGGCTCCAGTATTAATGAA	3300
QY	3301	TAGGTTCCAGTGATGAAAACATTTCAAGAGAACATGAGTGAAGACAGAGGCGCAAAATTTGA	3360
Db	3301	TAGGTTCCAGTGATGAAAACATTTCAAGAGAACATGAGTGAAGACAGAGGCGCAAAATTTGA	3360
QY	3361	ATGCTATGCTTAGATTTAGGGGTTTTTGGCAACTGAGGCTATATAACAAAGTCTTCTCGGAA	3420
Db	3361	ATGCTATGCTTAGATTTAGGGGTTTTTGGCAACTGAGGCTATATAACAAAGTCTTCTCGGAA	3420
QY	3421	GTAATTTGAACCATCTCGAAATTAACAAAAGCAAGATATGAGAAAGTAGTTCAGACTGTTA	3480
Db	3421	GTAATTTGAACCATCTCGAAATTAACAAAAGCAAGATATGAGAAAGTAGTTCAGACTGTTA	3480
QY	3481	ATACAGATTTCTCTCCATATCTGATTTCAAGTAACTTATGAAACAGGCTATGGGAATGATC	3540
Db	3481	ATACAGATTTCTCTCCATATCTGATTTCAAGTAACTTATGAAACAGGCTATGGGAATGATC	3540
QY	3541	ATGCATCTCAGGTTGTTCTGAGACCTGTAGACCTGTTGATGATGATGGTAAATTAAGG	3600
Db	3541	ATGCATCTCAGGTTGTTCTGAGACCTGTAGACCTGTTGATGATGATGGTAAATTAAGG	3600
QY	3601	AAGATCTAGTTTCTGCGAAATATACATTAAGAAAAGTTCTGCTGTTTTTGAACAAACG	3660
Db	3601	AAGATCTAGTTTCTGCGAAATATACATTAAGAAAAGTTCTGCTGTTTTTGAACAAACG	3660
QY	3661	TCACAGAGAGAGCTTAGCAGAGTCCCTTACACCATPACATTTGGCTCAGG	3720

QY	4801	CCCGTTCCTGGAAATCTGGAAATCAAGCCTCTTCTCTGATGACCTTGAATCTGAATCTTCTG	4860
Db	4801	CCCCCTTACCTGGAAATCTGGAAATCAAGCCTCTTCTCTGATGACCTTGAATCTGAATCTTCTG	4860
QY	4861	AAGCACAAGCCCCAGAGTCAAGCTCGTGTGGCAACATACATCTTCAACCTCTGCATTTGA	4920
Db	4861	AAGCACAAGCCCCAGAGTCAAGCTCGTGTGGCAACATACATCTTCAACCTCTGCATTTGA	4920
QY	4921	AAGTTCGCCAATTGAAGTTGCAGAATCTGCCAGAGGTCCAGCTGCTCATACTGA	4980
Db	4921	AAGTTCGCCAATTGAAGTTGCAGAATCTGCCAGAGGTCCAGCTGCTCATACTGA	4980
QY	4981	ATATCTGCTGGGTATATATGCAATGGAGAAAGTGTAGCAGAGGAGAGAGCCGAATTGACAG	5040
Db	4981	ATATCTGCTGGGTATATATGCAATGGAGAAAGTGTAGCAGAGGAGAGAGCCGAATTGACAG	5040
QY	5041	CTTCAACAGAAAGGGTCAACAAAGAAATGTCATGTGGTGTCTGGCTGACACCCCAAG	5100
Db	5041	CTTCAACAGAAAGGGTCAACAAAGAAATGTCATGTGGTGTCTGGCTGACACCCCAAG	5100
QY	5101	AATTATGCTCGTGTACAGTTTGGCCAGAAAACCAACATCACTTAACTAATCTAATTA	5160
Db	5101	AATTATGCTCGTGTACAGTTTGGCCAGAAAACCAACATCACTTAACTAATCTAATTA	5160
QY	5161	CTGAAGAGACTACTCATGTGTTGTTATGAAAACAGATGCTGAGTTGTGTGTGAACGACAC	5220
Db	5161	CTGAAGAGACTACTCATGTGTTGTTATGAAAACAGATGCTGAGTTGTGTGTGAACGACAC	5220
QY	5221	TGAAATTTTTTTCTAGAAATTCGGCGAGAGAAAATGGGTAGTTACTATATTTCTGGGTGACC	5280
Db	5221	TGAAATTTTTTTCTAGAAATTCGGCGAGAGAAAATGGGTAGTTACTATATTTCTGGGTGACC	5280
QY	5281	AGCTATTTAAAGAAAGAAAATGCTGAATGAGCATGTTTGAAGTCAGAGAGATGTGG	5340
Db	5281	AGCTATTTAAAGAAAGAAAATGCTGAATGAGCATGTTTGAAGTCAGAGAGATGTGG	5340
QY	5341	TCAATGGAAGAAACCAACCAAGTCCAAAGCAGACAGAGAATCCACAGACAGAAAGATCT	5400
Db	5341	TCAATGGAAGAAACCAACCAAGTCCAAAGCAGACAGAGAATCCACAGACAGAAAGATCT	5400
QY	5401	TCAGGGGGCTAGAAATCTGTTGCTATGGGCCCTTCAACCAATGCCCCAGATCAACTGG	5460
Db	5401	TCAGGGGGCTAGAAATCTGTTGCTATGGGCCCTTCAACCAATGCCCCAGATCAACTGG	5460
QY	5461	AATGGAATGATCAAGCTGTGTGTGCTTCTGTGGTGAAGAGACTTTATCATTTACACCTTG	5520
Db	5461	AATGGAATGATCAAGCTGTGTGTGCTTCTGTGGTGAAGAGACTTTATCATTTACACCTTG	5520
QY	5521	GCAAGAGTGTCCACCAATGTGGTTGTGACGCAGATGCTGTGACAGAGACAAATGGCT	5580
Db	5521	GCAAGAGTGTCCACCAATGTGGTTGTGACGCAGATGCTGTGACAGAGACAAATGGCT	5580
QY	5581	TCCATGCAATTTGGGCGAGATGTGTGAGGACCTGTGTGTGACCCGAGAGTGGGTGTGGACA	5640
Db	5581	TCCATGCAATTTGGGCGAGATGTGTGAGGACCTGTGTGTGACCCGAGAGTGGGTGTGGACA	5640
QY	5641	GTTGAGCACTCTACCAAGTGCACAGAGCTGACACCTAATCTGATACCCCAAGATCCCCACA	5700
Db	5641	GTTGAGCACTCTACCAAGTGCACAGAGCTGACACCTAATCTGATACCCCAAGATCCCCACA	5700
QY	5701	GCCACTACTGA 5711	
Db	5701	GCCACTACTGA 5711	

RESULT 11  
 US-08-658-322-1  
 ; Sequence 1, Application US/08658322  
 ; Patent No. 5863245  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Yeung, Anthony T.  
 ; TITLE OF INVENTION: Mismatch Endonuclease And Its Use in

TITLE OF INVENTION: Identifying Mutations In Targeted Polynucleotide Strands  
NUMBER OF SEQUENCES: 13  
CORRESPONDENCE ADDRESSES: 13  
ADDRESS: Dann, Dorfman, Herrell and Skillman, P.C.  
STREET: 1601 Market Street, Suite 720  
CITY: Philadelphia  
STATE: PA  
COUNTRY: USA  
ZIP: 19103-2307  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/658,322  
FILING DATE: 05-JUN-1996  
CLASSIFICATION: 435  
ATTORNEY/AGENT INFORMATION:  
NAME: Hagan, Patrick J.  
REGISTRATION NUMBER: 27,643  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (215) 563-4100  
TELEFAX: (215) 563-4044  
INFORMATION FOR SEQ ID NO: 1:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 5711 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: double  
TOPOLOGY: not relevant  
MOLECULE TYPE: DNA (genomic)  
HYPOTHETICAL: NO  
ANTI-SENSE: NO  
US-08-658-322-1

Query Match 99.8%; Score 5699.8; DB 2; Length 5711;  
Best Local Similarity 99.9%; Pred. No. 0;  
Matches 5704; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

QY 1 AGCTGCGTGAAGACTTCCGGAACCCGACACAGGCTGTGGGTTCTCAGATPACTGGGCC 60  
DB 1 AGCTGCGTGAAGACTTCCGGAACCCGACACAGGCTGTGGGTTCTCAGATPACTGGGCC 60  
QY 61 CCTGGGCTCAGAGGCTTCAACCTCTGCTGTGGGTAAGTTCAATTGGAACAGAAAGAA 120  
DB 61 CCTGGGCTCAGAGGCTTCAACCTCTGCTGTGGGTAAGTTCAATTGGAACAGAAAGAA 120  
QY 121 TGAATTTATCTGCTCTTGGCGTTGAAGAAAGTACAAATGTCAATTAATGTCAGAAAA 180  
DB 121 TGAATTTATCTGCTCTTGGCGTTGAAGAAAGTACAAATGTCAATTAATGTCAGAAAA 180  
QY 181 TCTTAAGATGTCCTATCTGTCTGAGTGTGATCAAGAACTGTCTCCCAAAAGTGTACC 240  
DB 181 TCTTAAGATGTCCTATCTGTCTGAGTGTGATCAAGAACTGTCTCCCAAAAGTGTACC 240  
QY 241 ACATATTTTGAAGATTTTGAAGCTGAAGCTTCTCAACCAAGAAAGAGGCTTCAAGT 300  
DB 241 ACATATTTTGAAGATTTTGAAGCTGAAGCTTCTCAACCAAGAAAGAGGCTTCAAGT 300  
QY 301 GTCTTTATGTAAGATGATATTAACCAAAAGAGCTTCAAGAAAGTACGAGATTAGTC 360  
DB 301 GTCTTTATGTAAGATGATATTAACCAAAAGAGCTTCAAGAAAGTACGAGATTAGTC 360  
QY 361 AACTGTTGAAGAGTATGAAAAATCAATTTGTGCTTTACGCTTGAACACAGTTTGGAGT 420  
DB 361 AACTGTTGAAGAGTATGAAAAATCAATTTGTGCTTTACGCTTGAACACAGTTTGGAGT 420  
QY 421 ATGCAAAAGAGCTATATTTTGAAGAAAGAAATTAATCTCTCGTAAGATCTAAAGATG 480  
DB 421 ATGCAAAAGAGCTATATTTTGAAGAAAGAAATTAATCTCTCGTAAGATCTAAAGATG 480  
QY 481 AAGTTTATCATCCAAAGTATGGGCTACAGAAACGTCGCAAAAGACTTCTACAGAGTG 540  
DB 481 AAGTTTATCATCCAAAGTATGGGCTACAGAAACGTCGCAAAAGACTTCTACAGAGTG 540

DB 481 AAGTTTATCATCCAAAGTATGGGCTACAGAAACGTCGCAAAAGACTTCTACAGAGTG 540  
QY 541 AACCAGAAATCTTCCCTTGAGAGAAACAGTCTCAAGTCCAACTCTCAACCTTGAA 600  
DB 541 AACCAGAAATCTTCCCTTGAGAGAAACAGTCTCAAGTCCAACTCTCAACCTTGAA 600  
QY 601 CTGTGAGAACTCTGAGGCAAAAGCAGGATACAACTCAAAAGACGTCTGTCTACATG 660  
DB 601 CTGTGAGAACTCTGAGGCAAAAGCAGGATACAACTCAAAAGACGTCTGTCTACATG 660  
QY 661 AATTGGATCTGATTTCTTGAAGATACCTTAATTAAGCACTTAATTGCGTGGAG 720  
DB 661 AATTGGATCTGATTTCTTGAAGATACCTTAATTAAGCACTTAATTGCGTGGAG 720  
QY 721 ATCAAGATGTACAATCAACCTCAAGGAACAGGATGAATCAGTTGGATTCTG 780  
DB 721 ATCAAGATGTACAATCAACCTCAAGGAACAGGATGAATCAGTTGGATTCTG 780  
QY 781 CAAAAAGGCTGTTGAAATTTTCTGAGACGATGTAACTGAATCATCATCAAC 840  
DB 781 CAAAAAGGCTGTTGAAATTTTCTGAGACGATGTAACTGAATCATCATCAAC 840  
QY 841 CCAATTAATGATTTTGAACCACTGAGAAAGCTGCTGAGAGGCTCAGAAAGT 900  
DB 841 CCAATTAATGATTTTGAACCACTGAGAAAGCTGCTGAGAGGCTCAGAAAGT 900  
QY 901 ATCAGGGATGTTCTGTTCAACTGATGAGGATGAGCAATGAGCAAACTCATGCA 960  
DB 901 ATCAGGGATGTTCTGTTCAACTGATGAGGATGAGCAATGAGCAAACTCATGCA 960  
QY 961 GCTGATTAACAGCATGAGAAACAGCAGTTTACTCACTAAAGACAGATGATAGAA 1020  
DB 961 GCTGATTAACAGCATGAGAAACAGCAGTTTACTCACTAAAGACAGATGATAGAA 1020  
QY 1021 AGCTGAATTTGTAATTAAGCAACAGCTGCTTACAGAGGCCAATATACAGAT 1080  
DB 1021 AGCTGAATTTGTAATTAAGCAACAGCTGCTTACAGAGGCCAATATACAGAT 1080  
QY 1081 GGGCTGAAGTAAAGAAACATGTAATGATGAGGAGACTCCAGACAGAAAAAGTAG 1140  
DB 1081 GGGCTGAAGTAAAGAAACATGTAATGATGAGGAGACTCCAGACAGAAAAAGTAG 1140  
QY 1141 ATCTGAATGCTGATCCCTGTGTGAGAGAAAGATGAAATAGCAGAACTGCATGCT 1200  
DB 1141 ATCTGAATGCTGATCCCTGTGTGAGAGAAAGATGAAATAGCAGAACTGCATGCT 1200  
QY 1201 CAGAGATCTTAAGATTAAGATGTTCTTGGATTAACCTTAATAGCAGATTGCA 1260  
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Db 5701 GCCACTACTGA 5711

RESULT 12  
US-08-603-753D-1  
; Sequence 1, Application US/08603753D  
; Patent No. 5891857  
; GENERAL INFORMATION:  
; APPLICANT: HOLT, JEFFREY T.  
; APPLICANT: JENSEN, ROY A.  
; APPLICANT: PAGE, DAVID L.  
; APPLICANT: KING, MARY-CLAIRE  
; APPLICANT: SZABO, CSILLA I.  
; APPLICANT: JETTON, THOMAS L.  
; APPLICANT: ROBINSON-BENION, CHERYL L.  
; APPLICANT: THOMPSON, MARILYN E.  
; TITLE OF INVENTION: CHARACTERIZED BRCA1 AND BRCA2

TITLE OF INVENTION: PROTEINS AND SCREENING AND THERAPEUTIC METHODS BASED ON  
TITLE OF INVENTION: CHARACTERIZED BRCA1 AND BRCA2 PROTEINS.  
NUMBER OF SEQUENCES: 29  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: ARLES A. TAYLOR, JR.  
STREET: SUITE 1401, UNIVERSITY TOWER, 3100 TOWER  
CITY: DURHAM  
STATE: NORTH CAROLINA  
COUNTRY: USA  
ZIP: 27707  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Diskette, 3.50 inch, 800 kb storage  
COMPUTER: IBM PC/XT/AT compatible  
OPERATING SYSTEM: Windows 3.1  
SOFTWARE: WORD PERFECT 6.1 and ASCII  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/603,753D  
FILING DATE: 20 FEB 1996  
CLASSIFICATION: 514  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: U.S. 08/373,799  
FILING DATE: 17 JAN 1995  
ATTORNEY/AGENT INFORMATION:  
NAME: ARLES A. TAYLOR, JR.  
REGISTRATION NUMBER: 39,395  
REFERENCE/DOCKET NUMBER: 1242/2  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (919) 493-8000  
TELEFAX: (919) 419-0383  
TELEX:  
INFORMATION FOR SEQ ID NO: 1:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 5712  
TYPE: nucleic acid  
STRANDEDNESS: double  
TOPOLOGY: linear  
MOLECULE TYPE: cDNA to mRNA  
HYPOTHETICAL: no  
ANTI-SENSE: no  
ORIGINAL SOURCE:  
ORGANISM: Homo sapiens  
INDIVIDUAL ISOLATE:  
DEVELOPMENTAL STAGE: adult  
TISSUE TYPE: female breast  
CELL TYPE: ductal carcinoma in situ, invasive  
CELL TYPE: breast cancer and normal breast tissue  
CELL LINE: not derived from a cell line  
ORGANELLE: no  
IMMEDIATE SOURCE:  
LIBRARY: cDNA library derived from human  
CLONE: obtained using published sequence  
POSITION IN GENOME:  
CHROMOSOME/SEGMENT: unknown  
MAP POSITION: unknown  
UNITS: unknown  
FEATURE:  
NAME/KEY: BRCA1  
LOCATION: Genbank accession no. U14680  
IDENTIFICATION METHOD: microscopically directed  
IDENTIFICATION METHOD: sampling and nuclease protection assay  
OTHER INFORMATION: gene encoding BRCA1 protein  
PUBLICATION INFORMATION:  
AUTHORS: Miki, Y., et. al.  
TITLE: A strong candidate gene for the breast and  
TITLE: ovarian cancer susceptibility gene BRCA1.  
JOURNAL: Science  
VOLUME: 266  
PAGES: 66-71  
DATE: 1994  
RELEVANT RESIDUES IN SEQ ID NO: 1:  
US-08-603-753D-1

Query Match 99.8%; Score 5699.8; DB 2; Length 5712;  
Best Local Similarity 99.9%; Pred. No. 0;  
Matches 5704; Conservative 0; Mismatches 7; Indels 0; Gaps 0;  
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## RESULT 13

US-09-099-753-1

Sequence 1, Application US/09099753

Patent No. 6149903

GENERAL INFORMATION:

APPLICANT: HOLT, JEFFREY T.

APPLICANT: JENSEN, ROY A.

APPLICANT: PAGE, DAVID L.

APPLICANT: KING, MARY-CLAIRE

APPLICANT: SZABO, CSILLA I.

APPLICANT: JETTON, THOMAS L.

APPLICANT: ROBINSON-BENION, CHERYL L.

APPLICANT: THOMPSON, MARILYN E.

TITLE OF INVENTION: CHARACTERIZED BRCA1 AND BRCA2

TITLE OF INVENTION: PROTEINS AND SCREENING AND THERAPEUTIC METHODS BASED ON

TITLE OF INVENTION: CHARACTERIZED BRCA1 AND BRCA2 PROTEINS.

NUMBER OF SEQUENCES: 29

CORRESPONDENCE ADDRESS:

ADDRESSEE: ARLES A. TAYLOR, JR.

STREET: SUITE 1401, UNIVERSITY TOWER, 3100 TOWER

CITY: DURHAM

STATE: NORTH CAROLINA

COUNTRY: USA

ZIP: 27707

COMPUTER READABLE FORM:

MEDIUM TYPE: Diskette, 3.50 inch, 800 kb storage

COMPUTER: IBM PC/XT/AT compatible

OPERATING SYSTEM: Windows 3.1

SOFTWARE: WORD PERFECT 6.1 and ASCII

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/099,753

FILING DATE:

CLASSIFICATION:

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 08/603,753

FILING DATE: 20 FEB 1996

APPLICATION NUMBER: U.S. 08/373,799

FILING DATE: 17 JAN 1995

ATTORNEY/AGENT INFORMATION:

NAME: ARLES A. TAYLOR, JR.

REGISTRATION NUMBER: 39,395

REFERENCE/DOCKET NUMBER: 1242/2

TELECOMMUNICATION INFORMATION:

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TELEFAX: (919) 419-0383

TELEX:

INFORMATION FOR SEQ ID NO: 1:

SEQUENCE CHARACTERISTICS:

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/      LENGTH: 5712
/      TYPE: nucleic acid
/      STRANDEDNESS: double
/      TOPOLOGY: linear
/      MOLECULE TYPE: cDNA to mRNA
/      HYPOTHETICAL: no
/      ANTI-SENSE: no
/      ORIGINAL SOURCE:
/      ORGANISM: Homo sapiens
/      INDIVIDUAL ISOLATE:
/      DEVELOPMENTAL STAGE: adult
/      TISSUE TYPE: female breast
/      CELL TYPE: ductal carcinoma in situ, invasive
/      CELL TYPE: breast cancer and normal breast tissue
/      CELL LINE: not derived from a cell line
/      ORGANELLE: no
/      IMMEDIATE SOURCE:
/      LIBRARY: cDNA library derived from human
/      CLONE: obtained using published sequence
/      POSITION IN GENOME:
/      CHROMOSOME/SEGMENT: unknown
/      MAP POSITION: unknown
/      UNITS: unknown
/      FEATURE:
/      NAME/KEY: BRCA1
/      LOCATION: GenBank accession no. U14680
/      IDENTIFICATION METHOD: microscopically directed
/      IDENTIFICATION METHOD: sampling and nuclease protection assay
/      OTHER INFORMATION: gene encoding BRCA1 protein
/      PUBLICATION INFORMATION:
/      AUTHORS: Miki, Y., et. al.
/      TITLE: A strong candidate gene for the breast and
/      TITLE: ovarian cancer susceptibility gene BRCA1.
/      JOURNAL: Science
/      VOLUME: 266
/      PAGES: 66-71
/      DATE: 1994
/      RELEVANT RESIDUES IN SEQ ID NO: 1:
/      US-09-099-753-1

Query Match      99.8%; Score 5699.8; DB 3; Length 5712;
Best Local Similarity 99.9%; Pred. No. 0;
Matches 5704; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

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Qy 1861 AAACGAAAGCTGAACCTTAAGACAGATATAGCAATATGAACTCGAATTTAAATATCC 1920  
Db 1861 AAACGAAAGCTGAACCTTAAGACAGATATAGCAATATGAACTCGAATTTAAATATCC 1920  
Qy 1921 ACAATTCAAAAGCACTTAAGAAATAGCTGAGAGAACTCTTACCGAGCATATTC 1980  
Db 1921 ACAATTCAAAAGCACTTAAGAAATAGCTGAGAGAACTCTTACCGAGCATATTC 1980  
Qy 1981 ATGCGCTTGAATCTGATGATGATGATGATGATGATGATGATGATGATGATG 2040  
Db 1981 ATGCGCTTGAATCTGATGATGATGATGATGATGATGATGATGATGATGATG 2040  
Qy 2041 TTGATAGTTGTTCTAGCAGTGAAGATTAAGAAAAGATTAACCAATGCCAGTCA 2100  
Db 2041 TTGATAGTTGTTCTAGCAGTGAAGATTAAGAAAAGATTAACCAATGCCAGTCA 2100  
Qy 2101 GGCACAGGAAACCTTAACATCTGAGAAAGTAAAGAACTCTGCACTGAGACCAAGAAAG 2160  
Db 2101 GGCACAGGAAACCTTAACATCTGAGAAAGTAAAGAACTCTGCACTGAGACCAAGAAAG 2160  
Qy 2161 GTAACCAAGCAATGAACAGCAAGTAAAGACATGACATGATGATCTTCCAGAGCTGA 2220  
Db 2161 GTAACCAAGCAATGAACAGCAAGTAAAGACATGACATGATGATCTTCCAGAGCTGA 2220  
Qy 2221 AGTTAACCAATGCACTGCTGTTCTTTACTAAGTGTCTCAATACAGTGAATTAAGAT 2280  
Db 2221 AGTTAACCAATGCACTGCTGTTCTTTACTAAGTGTCTCAATACAGTGAATTAAGAT 2280  
Qy 2281 TTGTCAATCTGATGCTTCAAGAGAGAAAGAAAGAACTGAGAAACAGTTAAAGTGT 2340  
Db 2281 TTGTCAATCTGATGCTTCAAGAGAGAAAGAAAGAACTGAGAAACAGTTAAAGTGT 2340  
Qy 2341 CTAATTAATGCTGAAGAACCCCAAGATCTCATGTTAAGTGAAGAAAGGTTTGGCAATG 2400  
Db 2341 CTAATTAATGCTGAAGAACCCCAAGATCTCATGTTAAGTGAAGAAAGGTTTGGCAATG 2400  
Qy 2401 AAAGATCTGTAGAGATGAGATTTTCACTGATGATCTGATGATGATGATGATG 2460  
Db 2401 AAAGATCTGTAGAGATGAGATTTTCACTGATGATCTGATGATGATGATGATG 2460  
Qy 2461 AAAGATCTGTGATGATGATGATGATGATGATGATGATGATGATGATGATG 2520  
Db 2461 AAAGATCTGTGATGATGATGATGATGATGATGATGATGATGATGATGATG 2520  
Qy 2521 GTGTAGTCAAGTGAAGATTTGAAACCCCAAGGAGCTAATTCATGATGATGATG 2580  
Db 2521 GTGTAGTCAAGTGAAGATTTGAAACCCCAAGGAGCTAATTCATGATGATGATG 2580  
Qy 2581 ATATATGAATGACACAGAAAGCTTTAATGATGATGATGATGATGATGATGATG 2640  
Db 2581 ATATATGAATGACACAGAAAGCTTTAATGATGATGATGATGATGATGATGATG 2640

QY	2641	UGGAAACACAGCATAGAAATGGAAGAAAGTGAACCTGATGCTCAGATATTTGCAAGATACAT	2700
Db	2641	GGGAAACAGACATAGAAATGGAAGAAAGTGAACCTGATGCTCAGATATTTGCAAGATACAT	2700
QY	2701	TCAAGGTTTCAAAGGCGCAGTCAATTTGCTGTTTTCAAATCCAGAAATCCAGAAGAG	2760
Db	2701	TCAAGGTTTCAAAGGCGCAGTCAATTTGCTGTTTTCAAATCCAGAAATCCAGAAGAG	2760
QY	2761	AATGTGCAACATTTCTGCGCCACTGTGGGTCTTTAAAGAAACAAAGTCCAAAGTCACTT	2820
Db	2761	AATGTGCAACATTTCTGCGCCACTGTGGGTCTTTAAAGAAACAAAGTCCAAAGTCACTT	2820
QY	2821	TTGAATGTGCAACAAAGAGAAATTCAGGAAAGAGAGCTTAATTCAGGCTGTAC	2880
Db	2821	TTGAATGTGCAACAAAGAGAAATTCAGGAAAGAGAGCTTAATTCAGGCTGTAC	2880
QY	2881	AGACAGTTAATATCACTGACAGGCTTCTGTGTTGGTCAGAAAGATAGCCAGTTGATA	2940
Db	2881	AGACAGTTAATATCACTGACAGGCTTCTGTGTTGGTCAGAAAGATAGCCAGTTGATA	2940
QY	2941	ATGCCAAATGTAGATACAAAGAGGCTCTAGGTTTGTCTATCATCTCAGTTCAGAGCA	3000
Db	2941	ATGCCAAATGTAGATACAAAGAGGCTCTAGGTTTGTCTATCATCTCAGTTCAGAGCA	3000
QY	3001	ACGAAACCTGACCTCACTTCTCCAAATAAACATGACCTTTTACAAACCCTATGTGTATC	3060
Db	3001	ACGAAACCTGACCTCACTTCTCCAAATAAACATGACCTTTTACAAACCCTATGTGTATC	3060
QY	3061	CACCACTTTTCCCATCAAGTCAATTTGTTAAACTTAAATGTAGAAAATCTGCTAGAG	3120
Db	3061	CACCACTTTTCCCATCAAGTCAATTTGTTAAACTTAAATGTAGAAAATCTGCTAGAG	3120
QY	3121	AAAACTTGAAGAAACATTCATGTCACTGAGAAAGAAATGAGAAATGAGAAACATTC	3180
Db	3121	AAAACTTGAAGAAACATTCATGTCACTGAGAAAGAAATGAGAAATGAGAAACATTC	3180
QY	3181	GTACAGTGAACAATTAGCCGTATTAACATTTAGAAAATGTTTTTAAAGAGCCAGCT	3240
Db	3181	GTACAGTGAACAATTAGCCGTATTAACATTTAGAAAATGTTTTTAAAGAGCCAGCT	3240
QY	3241	CAAGCAATTAATTAAGAACTAGGTTCCCACTAATGAATGGGCTCCAGTATTTATGAA	3300
Db	3241	CAAGCAATTAATTAAGAACTAGGTTCCCACTAATGAATGGGCTCCAGTATTTATGAA	3300
QY	3301	TAGGTTCCAGTATGAAAAACATTCAGCAGAACTAGTAGAGAAACAGAGGCGCAAAATTTGA	3360
Db	3301	TAGGTTCCAGTATGAAAAACATTCAGCAGAACTAGTAGAGAAACAGAGGCGCAAAATTTGA	3360
QY	3361	ATGCTATGCTTAGATTAGGGGTTTTGCACTGAGGTCTATTAACAAAGTCTTCTTGAA	3420
Db	3361	ATGCTATGCTTAGATTAGGGGTTTTGCACTGAGGTCTATTAACAAAGTCTTCTTGAA	3420
QY	3421	GTAATTTGTAACATCTCTGAATTAATAAAAGCAAGATATGAGAGAGTGTGAGCTGTTA	3480
Db	3421	GTAATTTGTAACATCTCTGAATTAATAAAAGCAAGATATGAGAGAGTGTGAGCTGTTA	3480
QY	3481	ATACAGATTTCTCTCCATATCTGATTTCAAGTAACTTGTGAACAGCTTATGGGAAGTATC	3540
Db	3481	ATACAGATTTCTCTCCATATCTGATTTCAAGTAACTTGTGAACAGCTTATGGGAAGTATC	3540
QY	3541	ATGCACTCAGGTTTGTCTGAGACACTGATGACCTGTATGATGATGGTAAATTAAG	3600
Db	3541	ATGCACTCAGGTTTGTCTGAGACACTGATGACCTGTATGATGATGGTAAATTAAG	3600
QY	3601	AAGATTAAGTTTGTCTGAAAAATGACATTAAGAAAGTGTGCTGTTTTTGAAGAAAGCG	3660
Db	3601	AAGATTAAGTTTGTCTGAAAAATGACATTAAGAAAGTGTGCTGTTTTTGAAGAAAGCG	3660
QY	3661	TTCCAGAGAGAGGATTAGCAGAGTCTTAGCCCTTTTCAACCCTATCACTTTGGCTCAG	3720
Db	3661	TTCCAGAGAGAGGATTAGCAGAGTCTTAGCCCTTTTCAACCCTATCACTTTGGCTCAG	3720

QY	3721	TTTACCCGAAGGGGGCCAAAGAAATTAAAGTCTCTCAGAAAGACAATTATCTAGTAGAGTG	3780
Db	3721	GTTCACGAAGGGGGCCAAAGAAATTAAAGTCTCTCAGAAAGACAATTATCTAGTAGAGTG	3780
QY	3781	AAGAGCTTCCCTGCTCCAAACACTTGTTATTTGGTAAAGTAAACAATTTACCTTCTCAGT	3840
Db	3781	AAGAGCTTCCCTGCTCCAAACACTTGTTATTTGGTAAAGTAAACAATTTACCTTCTCAGT	3840
QY	3841	CTACTAGGCATAGCACCGTTGCTACCGAGTGTCTGTCTTAAGACAACAAGGAGAAATTTAT	3900
Db	3841	CTACTAGGCATAGCACCGTTGCTACCGAGTGTCTGTCTTAAGACAACAAGGAGAAATTTAT	3900
QY	3901	TATCATTTGAAGAAATAGCTTAAATTAAGTCTGCACTAACCAAGTAAATTTGGCAAAAGCATCTC	3960
Db	3901	TATCATTTGAAGAAATAGCTTAAATTAAGTCTGCACTAACCAAGTAAATTTGGCAAAAGCATCTC	3960
QY	3961	AGGAACATCACCTTAGTAGAGGAAACAAATTTTCGTAGCTTGTTTTCTTCAAGTGTCA	4020
Db	3961	AGGAACATCACCTTAGTAGAGGAAACAAATTTTCGTAGCTTGTTTTCTTCAAGTGTCA	4020
QY	4021	GTGAATTGGAAGACTTGACTGCAAAATCAAAACCCAGAGTCCCTTCTTGAATTGGTCTT	4080
Db	4021	GTGAATTGGAAGACTTGACTGCAAAATCAAAACCCAGAGTCCCTTCTTGAATTGGTCTT	4080
QY	4081	CCAAACAATAGGCACTGACTGTGAAGCCAGGAGTGTGTCTGAGTGTCAAGAATTTGG	4140
Db	4081	CCAAACAATAGGCACTGACTGTGAAGCCAGGAGTGTGTCTGAGTGTCAAGAATTTGG	4140
QY	4141	TTTCAGATGATGAAGAAAGAAACGGGCTTGGAAAGAAATTAATCAGAAGACGAAGACA	4200
Db	4141	TTTCAGATGATGAAGAAAGAAACGGGCTTGGAAAGAAATTAATCAGAAGACGAAGACA	4200
QY	4201	TGGAATTCAAACTTAGTGTAAGCAAGCATCTGGGTGTGAGTGAACAAAGCCTCTCTGAG	4260
Db	4201	TGGAATTCAAACTTAGTGTAAGCAAGCATCTGGGTGTGAGTGAACAAAGCCTCTCTGAG	4260
QY	4261	ACTGCTCAGGGCTATTCCTCTGAGTGTACATTTTAACCACTCAGCAGAGGATACCATGC	4320
Db	4261	ACTGCTCAGGGCTATTCCTCTGAGTGTACATTTTAACCACTCAGCAGAGGATACCATGC	4320
QY	4321	AACATAACCTGATTAAGCTCCAGAGGAAATGGGTGAACCTAGAGCTGTGTTAAACAGC	4380
Db	4321	AACATAACCTGATTAAGCTCCAGAGGAAATGGGTGAACCTAGAGCTGTGTTAAACAGC	4380
QY	4381	ATGGGAGCAGCCTTCTTAACAGTAAACCCTTCATCATTAAGTGACTCCTCTGACCCTTAGG	4440
Db	4381	ATGGGAGCAGCCTTCTTAACAGTAAACCCTTCATCATTAAGTGACTCCTCTGACCCTTAGG	4440
QY	4441	ACCTGCGAATTCAGAAACAAAGCATCAGAAAAAGAGATTTAACCTTCAAGAAAAGTA	4500
Db	4441	ACCTGCGAATTCAGAAACAAAGCATCAGAAAAAGAGATTTAACCTTCAAGAAAAGTA	4500
QY	4501	GTGAATACCTTATTAAGCCAGAAATCCAGAAAGGCCCTTTCGCTGTACAAGTTTAGAGTGTCTG	4560
Db	4501	GTGAATACCTTATTAAGCCAGAAATCCAGAAAGGCCCTTTCGCTGTACAAGTTTAGAGTGTCTG	4560
QY	4561	CAGATAGTCTTACACAGTAAAAATTAAGAACCAAGAGTGAAGAGGTCAATCCCTCTTAAT	4620
Db	4561	CAGATAGTCTTACACAGTAAAAATTAAGAACCAAGAGTGAAGAGGTCAATCCCTCTTAAT	4620
QY	4621	GCCCATCATTAAGATGATAGTGTGTACATGTCAAGTTGCTCTGGAGTCTTCAGAAATGAA	4680
Db	4621	GCCCATCATTAAGATGATAGTGTGTACATGTCAAGTTGCTCTGGAGTCTTCAGAAATGAA	4680
QY	4681	ACTAACCCATCTCAAGAGAGAGTCAATTAAAGTTGTGATGTGAGACCAACAGCTGGAAG	4740
Db	4681	ACTAACCCATCTCAAGAGAGAGTCAATTAAAGTTGTGATGTGAGACCAACAGCTGGAAG	4740
QY	4741	AGTCGGGCCCAACAGATTTTGAACGAAACATCTTACTTGCAAGGCAAGATCTAAGGGAA	4800
Db	4741	AGTCGGGCCCAACAGATTTTGAACGAAACATCTTACTTGCAAGGCAAGATCTAAGGGAA	4800
QY	4801	CCCCCTTACCTGGAATCTGGAATCAGCCTCTTCTCTGTAGTACCCTGAATCTGATCTTCTG	4860



Db 241 ACATATTTTGCMAATTTTGACGTGAAATCTTCAACCGAAGAAAGGCGCTTCAACGT 300  
Qy 301 GTCTTTATGTAAGAAATATTAACCAAAAGAGCTTCAAGAAAGTACGATTTTATC 360  
Db 301 GTCTTTATGTAAGAAATATTAACCAAAAGAGCTTCAAGAAAGTACGATTTTATC 360  
Qy 361 AACTTGTGAAGAGCTATTTGAAAATCATTTGTGCTTTCACTTGCACACAGTTTGGAGT 420  
Db 361 AACTTGTGAAGAGCTATTTGAAAATCATTTGTGCTTTCACTTGCACACAGTTTGGAGT 420  
Qy 421 ATGCAACAGCTATTAATTTTGCAAAAAAGAAAATTAATCTTCTGCAACATCTAAAGATG 480  
Db 421 ATGCAACAGCTATTAATTTTGCAAAAAAGAAAATTAATCTTCTGCAACATCTAAAGATG 480  
Qy 481 AAGTTTCTATCATCAAAAGTAAGGCTTACAAAACCGGCAAAAGACTTCTACAGATG 540  
Db 481 AAGTTTCTATCATCAAAAGTAAGGCTTACAAAACCGGCAAAAGACTTCTACAGATG 540  
Qy 541 AACCCGAAAATCTTCTTGCAGGAAACCACTCACTGTCCTCACTCTTAACTTGGAA 600  
Db 541 AACCCGAAAATCTTCTTGCAGGAAACCACTCACTGTCCTCACTCTTAACTTGGAA 600  
Qy 601 CTGTGAAGACTTGTGAAGCAAAAGACGCGGATCAACTCAAAAAGCTTGTCTTACATG 660  
Db 601 CTGTGAAGACTTGTGAAGCAAAAGACGCGGATCAACTCAAAAAGCTTGTCTTACATG 660  
Qy 661 AATGGGATCTGATTTCTTGAAGTACCGTTAATTAAGGCACTTATGCGATGGGAG 720  
Db 661 AATGGGATCTGATTTCTTGAAGTACCGTTAATTAAGGCACTTATGCGATGGGAG 720  
Qy 721 ATCAAGAAATGTTCAAAATCAACCCCTCAAGGACCAAGGATGAATCAGTTTGGATCTG 780  
Db 721 ATCAAGAAATGTTCAAAATCAACCCCTCAAGGACCAAGGATGAATCAGTTTGGATCTG 780  
Qy 781 CAAAAAAGGCTCTTGTGAATTTTCTGAAGCGATGTAACAAATCTGAACATCAAC 840  
Db 781 CAAAAAAGGCTCTTGTGAATTTTCTGAAGCGATGTAACAAATCTGAACATCAAC 840  
Qy 841 CCAGTAATTAATGATTTGAACAACAAGGAGCGGCTGAGAGGATCAAGAAAAGT 900  
Db 841 CCAGTAATTAATGATTTGAACAACAAGGAGCGGCTGAGAGGATCAAGAAAAGT 900  
Qy 901 ATCAAGGAGTCTTGTTCAAACTTGCATGTGAGCCATGTGCAAAATCTCATGCA 960  
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Qy 1021 AGGCTGAATTTCTGTAATTAAGCAAAACAGCTGGCTTGAAGAGGCAACATTAACGAT 1080  
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Qy 1141 ATCTGAATGCTGATCCCTGTGTGAGAGAAAAGATGGAATAGCAAGAACTGCCATGCT 1200  
Db 1141 ATCTGAATGCTGATCCCTGTGTGAGAGAAAAGATGGAATAGCAAGAACTGCCATGCT 1200  
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Db 1381 AATATCTGCTTCTTCAAGAAATATAGACTTACTGGCAGATGATCTCATAGGCTTTAA 1440  
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Db 1501 TTGGAAAACCTTATCGAAGAGGCAAGCTCCCAACTTAAAGCATGTAATCTGAAAATC 1560  
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Db 1561 TAAATTATGAGAGCTTTGTTACTGAGCAGATTAATCAAGAGCGTCCCTGCAATA 1620  
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Db 1621 AATTTAAGCGTAAAGAGACCTACATCAGGCTTCACTCTGAGATTTTATCAAGAAAG 1680  
Qy 1681 CAGATTTGGCAGTTCAAAAGACTCTGTAATGATTAATCAGGGAATTAACCAACGAGC 1740  
Db 1681 CAGATTTGGCAGTTCAAAAGACTCTGTAATGATTAATCAGGGAATTAACCAACGAGC 1740  
Qy 1741 AGAATGGTCAAGTATGATTAATTAATGATGCTGATGGAATTAACCAAGGATG 1800  
Db 1741 AGAATGGTCAAGTATGATTAATTAATGATGCTGATGGAATTAACCAAGGATG 1800  
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Db 1801 CTATTCAGAAATGAGAAAATCTTAACCAATAGATCACTGAAAAGAAATCTGCTTTCA 1860  
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Db 1921 ACAATTCAAAAGACCTTAAGAAATGAGGCTGAGAGGAAAGTCTTACACAGGATTC 1980  
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Db 2341 CTATATATGCTGAAGACCCCAAGATCTCATGTTAAGTGAAGAAAGGTTTGCAAAATG 2400  
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QY 2461 AAATATCTCGTACTGGAATGACACTCTAGGAGGCAAAAACAGAACCAATTAAT 2520  
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DB 3481 ATACAGATTTTCTCTCATATCTGATTTTCAAGTAACTTAAGAACAGCCTTAATGGAATGATC 3540  
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DB 3541 ATGCAATCAGGTTTGTCTGAGACCTGATGACCTGTATGATGATGTTGTAATTAAGG 3600  
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DB 3601 AAGATCTAGTGTGCTGTAATTAAGGAAAGTTCGCTGTTTATGACAAAGCG 3660  
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DB 3661 TCCAGAGGAGAGCTTGAAGAGAGTCTAGCCCTTCAACCATACATGATTTGGCTCAG 3720  
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DB 3721 GTTACCGAAGAGGAGGCGCAAGAAATTAAGAGTCCAGAGAAAGTATCTAGTGAAGT 3780  
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DB 4321 AACATTAACCTTAAGTTCAGCAGAAATGCTGAACCTAGAACCTGTGTTAGAACGC 4380  
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DB 4501 GTGAATTAACCTTAAGTTCAGAGATTCAGAGAGGCTTCTGCTGCAAGATTTGAGGTCTG 4560  
QY 4561 CAGATAGTTCTACAGTAAATTAAGAACCAAGAGTGAAGAGTCAATCCCTCTTAAT 4620  
DB 4561 CAGATAGTTCTACAGTAAATTAAGAACCAAGAGTGAAGAGTCAATCCCTCTTAAT 4620  
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Db 481 AAGTTCTATGATCCAAAGTAGGGCTACAGAAACCGTCCAAAAGACTTCTACAGATG 540  
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Search completed: December 14, 2003, 20:34:06  
Job time : 366 secs



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OM nucleic - nucleic search, using sw model

Run on: December 14, 2003, 11:42:27 ; Search time 1670 Seconds  
(without alignments)  
11365.913 Million cell updates/sec

Title: US-09-923-327a-263

Perfect score: 5711

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Scoring table: IDENTITY NUC

Gapop 10.0 , Gapext 1.0

Searched: 2201672 seqs, 1661799599 residues

Total number of hits satisfying chosen parameters: 4403344

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Published Applications NA:\*

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Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

## SUMMARIES

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2	5711	100.0	5711	11	US-09-982-828-1
3	5709.4	100.0	5711	10	US-09-734-672-5
4	5709.4	100.0	5711	11	US-09-982-828-3
5	5709.4	100.0	5711	15	US-10-022-819-1
6	5701.4	99.8	5711	10	US-09-734-672-3
7	5701.4	99.8	5711	11	US-09-982-828-5
8	5649.8	98.9	5709	13	US-10-240-965-268
9	595.4	10.4	597	13	US-10-029-386-12887
10	500.4	8.8	502	13	US-10-029-386-9876
11	416	7.3	505	13	US-10-029-386-2689
12	364.6	6.4	499	11	US-09-911-904-127
13	277	4.9	277	13	US-10-029-386-16389
14	201	3.5	369	13	US-10-286-628-39
15	173.8	3.0	424	9	US-09-864-761-4552

16	170	3.0	170	13	US-10-029-386-23576	Sequence 23576, A
17	145.4	2.5	147	9	US-09-864-761-21299	Sequence 21299, A
18	121	2.1	121	11	US-09-818-875-653	Sequence 653, App
19	121	2.1	121	11	US-09-818-875-654	Sequence 654, App
20	121	2.1	121	11	US-09-818-875-657	Sequence 657, App
21	121	2.1	121	11	US-09-818-875-658	Sequence 658, App
22	121	2.1	121	11	US-09-818-875-661	Sequence 661, App
23	121	2.1	121	11	US-09-818-875-662	Sequence 662, App
24	121	2.1	121	11	US-09-818-875-665	Sequence 665, App
25	121	2.1	121	11	US-09-818-875-666	Sequence 666, App
26	121	2.1	121	11	US-09-818-875-669	Sequence 669, App
27	121	2.1	121	11	US-09-818-875-670	Sequence 670, App
28	121	2.1	121	11	US-09-818-875-673	Sequence 673, App
29	121	2.1	121	11	US-09-818-875-674	Sequence 674, App
30	121	2.1	121	11	US-09-818-875-677	Sequence 677, App
31	121	2.1	121	11	US-09-818-875-678	Sequence 678, App
32	121	2.1	121	11	US-09-818-875-681	Sequence 681, App
33	121	2.1	121	11	US-09-818-875-682	Sequence 682, App
34	121	2.1	121	11	US-09-818-875-685	Sequence 685, App
35	121	2.1	121	11	US-09-818-875-686	Sequence 686, App
36	121	2.1	121	11	US-09-818-875-689	Sequence 689, App
37	121	2.1	121	11	US-09-818-875-690	Sequence 690, App
38	121	2.1	121	11	US-09-818-875-693	Sequence 693, App
39	121	2.1	121	11	US-09-818-875-694	Sequence 694, App
40	121	2.1	121	11	US-09-818-875-697	Sequence 697, App
41	121	2.1	121	11	US-09-818-875-698	Sequence 698, App
42	121	2.1	121	11	US-09-818-875-701	Sequence 701, App
43	121	2.1	121	11	US-09-818-875-702	Sequence 702, App
44	121	2.1	121	11	US-09-818-875-705	Sequence 705, App
45	121	2.1	121	11	US-09-818-875-706	Sequence 706, App

## ALIGNMENTS

RESULT 1  
US-09-734-672-1  
Sequence 1, Application US/09734672  
Publication No. US20020183268A1  
GENERAL INFORMATION:  
APPLICANT: Murphy, Patricia D.  
Alvarez, Antonette C.  
Critz, Brenda S.  
Olson, Sheri U.  
Schelter, Denise B.  
Zeng, Bin  
TITLE OF INVENTION: Coding Sequences of the Human  
BRCA1 Gene  
NUMBER OF SEQUENCES: 72  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Morgan Lewis & Bockius LLP  
STREET: 1111 Pennsylvania Ave., N.W.  
CITY: Washington  
STATE: District of Columbia  
COUNTRY: USA  
ZIP: 20004  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/734,672  
FILING DATE: 03-Dec-2000  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/966,436  
FILING DATE: 07-No. US20020183268A1-97  
APPLICATION NUMBER: US 08/598,591  
FILING DATE: 12-Feb-96  
ATTORNEY/AGENT INFORMATION:  
NAME: Michael S. Tuscan  
REGISTRATION NUMBER: 43,210

REFERENCE/DOCKET NUMBER: 44921-5055-02-US  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 202-739-3000  
TELEFAX: 202-739-3001  
INFORMATION FOR SEQ ID NO: 1:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 5711 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: No. US20020183268A1 Relevant  
TOPOLOGY: linear  
MOLECULE TYPE: cDNA  
ORIGINAL SOURCE:  
ORGANISM: Homo sapiens  
STRAIN: BRCA1  
POSITION IN GENOME:  
CHROMOSOME/SEGMENT: 17  
MAP POSITION: 17q21  
SEQUENCE DESCRIPTION: SEQ ID NO: 1:  
US-09-734-672-1

Query Match 100.0%; Score 5711; DB 10; Length 5711;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 5711; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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61 CCTGCGCTCAGAGAGCCCTTCAACCTCTGCTGTGGGTTAAAGTTCAATTGGAACGAAAGAA 120  
61 CCTGCGCTCAGAGAGCCCTTCAACCTCTGCTGTGGGTTAAAGTTCAATTGGAACGAAAGAA 120  
121 TGGATTTATCTGCTCTTGGCGTTGAAGAAGTCAATAATGCTATTAATGTCAGAA 180  
121 TGGATTTATCTGCTCTTGGCGTTGAAGAAGTCAATAATGCTATTAATGTCAGAA 180  
181 TCTTAGAGTGTCCCATCTGTCTGAGTTGATCAAGAACTGTCTCCAAAGTGTGACC 240  
181 TCTTAGAGTGTCCCATCTGTCTGAGTTGATCAAGAACTGTCTCCAAAGTGTGACC 240  
241 ACATATTTTGCAGAAATTTGCAATGCTGAAATCTTCAACGAGAGAAAGGCTTCAAGT 300  
241 ACATATTTTGCAGAAATTTGCAATGCTGAAATCTTCAACGAGAGAAAGGCTTCAAGT 300  
301 GTCCTTATGTAAGATGATATTAACCAAGAGGCTCAAGAAATGTAAGATTAAGT 360  
301 GTCCTTATGTAAGATGATATTAACCAAGAGGCTCAAGAAATGTAAGATTAAGT 360  
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361 AACTGTGAGAGGCTATGAAATCATTTGTGCTTTCACTTGAACAAGTTTGAGT 420  
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421 ATGCAACAGCTATTAATTTGCAAAAAGAAATTAATCTCTGTAACATCTAAAGATG 480  
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601 CTGTGAGAACTCTGAGCAAAAGCAGCGATCAAACTCAAAAGACGCTGTCTACATTTG 660  
661 AATTGGGATCTGATTTCTTGAAGTACCGTTAAATGAAGCACTTAATGCGAGTGGAG 720  
661 AATTGGGATCTGATTTCTTGAAGTACCGTTAAATGAAGCACTTAATGCGAGTGGAG 720  
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DB 721 ATCAAGATTTGTAACAATCAACCCTCAAGAACAGGATGAATGATTTGATTTCTG 780  
DB 781 CAAAAAGGCTGCTTGTGAATTTTCTGAGAGGATGTAACTAATCTGATCATCTAC 840  
DB 781 CAAAAAGGCTGCTTGTGAATTTTCTGAGAGGATGTAACTAATCTGATCATCTAC 840  
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DB 841 CCAGTAATTAATGATTTGAACCACTGAGAGCGGACGCTGAGAGGATCATCAGAAAGT 900  
DB 901 ATCAAGGATTTCTGTTTCAAACTTGAAGTGTGAGCCATGTGGACAATTAATCTAGCCA 960  
DB 901 ATCAAGGATTTCTGTTTCAAACTTGAAGTGTGAGCCATGTGGACAATTAATCTAGCCA 960  
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DB 961 GCTCATTAAGCATGAGAAACGAGTTTATTAATCTAATGAAGCAAGAAATGAATGAGAA 1020  
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DB 1141 ATCTGAATGCTGATCCCTGTGTGAGAGAAAGATGAATTAAGCAAAATCTGCAATGCT 1200  
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DB 1201 CAGAGAAATCTGAGATGCTGAGAGATGTTCTTGTGATTAAGCAATTAAGCAATGCTGAG 1260  
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DB 1261 AAGTTAATGAGTGTGTTTCCAGAGATGATGAATGTTAGTTCTGATGATCTCAATGATG 1320  
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DB 1321 GGGAGTCTGAATCAAAATGCCAAAGTGTGATGATGATGATGATGATGATGATGATG 1380  
DB 1381 AATATTCGTTCTTCAAGAGAAATGATGATGATGATGATGATGATGATGATGATGATG 1440  
DB 1381 AATATTCGTTCTTCAAGAGAAATGATGATGATGATGATGATGATGATGATGATGATG 1440  
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DB 1501 TTGGGAAACCTATTCGAGAGAGGCAAGCTCCCACTTAAGCAATGATGATGATGATGAT 1560  
DB 1561 TAATTAATGAGAGATTTGTTCTGAGCAAGATTAATCAAGAGGCTCCCTCAAAATA 1620  
DB 1561 TAATTAATGAGAGATTTGTTCTGAGCAAGATTAATCAAGAGGCTCCCTCAAAATA 1620  
DB 1621 AATTAAAGCGTAAAGAGACCTTCAATCAAGGCTTCAATCTGAGATTTTATCAAGAAAG 1680  
DB 1621 AATTAAAGCGTAAAGAGACCTTCAATCAAGGCTTCAATCTGAGATTTTATCAAGAAAG 1680  
DB 1681 CAGATTGGCAGTTCAAAAGACCTCTGAAATGATTAATCAGGGGAACTTAACCAAGCGAGC 1740  
DB 1681 CAGATTGGCAGTTCAAAAGACCTCTGAAATGATTAATCAGGGGAACTTAACCAAGCGAGC 1740  
DB 1741 AGAATGGCAAGTATGATTAATTAATGATGATGATGATGATGATGATGATGATGATGAT 1800  
DB 1741 AGAATGGCAAGTATGATTAATTAATGATGATGATGATGATGATGATGATGATGATGAT 1800  
DB 1801 CTATTCAGATGAGAAAAATCTTAACCAATGATGATGATGATGATGATGATGATGATGATGAT 1860  
DB 1801 CTATTCAGATGAGAAAAATCTTAACCAATGATGATGATGATGATGATGATGATGATGATGAT 1860



Db 1801 CTATTCAGAAATGAGAAAAATCTCTAACCCAAATAGAACTCGAAAAAGAAATCTGCTTTCA 1860  
Qy 1861 AAAGAAAAGCTGAACCTTAATAGCAGCAGTATATGAAATATGAACTCGAATTAATATCC 1920  
Db 1861 AAAGAAAAGCTGAACCTTAATAGCAGCAGTATATGAAATATGAACTCGAATTAATATCC 1920  
Qy 1921 ACAATTCAAAAGCACTTAAAAAGAAATAGCTGAGGAGAAAGTCTTCTACCAAGCATAATTC 1980  
Db 1921 ACAATTCAAAAGCACTTAAAAAGAAATAGCTGAGGAGAAAGTCTTCTACCAAGCATAATTC 1980  
Qy 1981 ATGGCTTGAACCTAGTATGCTAGTAAATCTTAAGCCCACTTAATGTACTGAATTCGAAA 2040  
Db 1981 ATGGCTTGAACCTAGTATGCTAGTAAATCTTAAGCCCACTTAATGTACTGAATTCGAAA 2040  
Qy 2041 TTGATAGTTGTTCTAGCAGTGAAGATTAAGAAAAAAGTAACAACCAATGCCAGTCA 2100  
Db 2041 TTGATAGTTGTTCTAGCAGTGAAGATTAAGAAAAAAGTAACAACCAATGCCAGTCA 2100  
Qy 2101 GGCAACAGCAGAAACCTTAACACTCATGGAAGGTAAAGAACTGCAACTGGAAGCCAGAAAGA 2160  
Db 2101 GGCAACAGCAGAAACCTTAACACTCATGGAAGGTAAAGAACTGCAACTGGAAGCCAGAAAGA 2160  
Qy 2161 GTAACAAAGCCAAATGACAGACAAAGTAAAGACATGACAGTGAATCTTTCCAGAGCTGA 2220  
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Qy 2221 AGTTAAACAATGCACTCTGCTTTCTTTACTAAGTGTCAATATCCAGTGAATCTTAAGAAAT 2280  
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Qy 2521 GTGTGAGTCACTGTGACAGCAATTTGAAAAACCCCAAGGGAATTAATTCATGCTTTCCAAAG 2580  
Db 2521 GTGTGAGTCACTGTGACAGCAATTTGAAAAACCCCAAGGGAATTAATTCATGCTTTCCAAAG 2580  
Qy 2581 ATTAATGAATGACACAGAAAGCTTTAATGATCCATTGGGACATGAAGTTAACCAAGTCC 2640  
Db 2581 ATTAATGAATGACACAGAAAGCTTTAATGATCCATTGGGACATGAAGTTAACCAAGTCC 2640  
Qy 2641 GGGAAAACAAGATGAAATGGAAGAAAGTGAACCTGATGCTAGTATTTGCAAGTAATCAT 2700  
Db 2641 GGGAAAACAAGATGAAATGGAAGAAAGTGAACCTGATGCTAGTATTTGCAAGTAATCAT 2700  
Qy 2701 TCAAGTTTCAAAAGCCAGTCAATTTGCTGTGTTTCAAAATCAGGAATGAGAAAGAG 2760  
Db 2701 TCAAGTTTCAAAAGCCAGTCAATTTGCTGTGTTTCAAAATCAGGAATGAGAAAGAG 2760  
Qy 2761 AATGTGCAACATTTCTGCTCCCACTCTGGGCTCTTAAGAAACAAAGTCCAAAGTCACTT 2820  
Db 2761 AATGTGCAACATTTCTGCTCCCACTCTGGGCTCTTAAGAAACAAAGTCCAAAGTCACTT 2820  
Qy 2821 TTGAATGGAACAAAGAAAGAAATCAAGGAAGAAAGTGAATGCTAATTCAGACCTGTAC 2880  
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Qy 2881 AGACAGTTAATATCACTGACAGGCTTTCTGTGTGTTGTCAAGAAAGATAGCAGTGTGATA 2940  
Db 2881 AGACAGTTAATATCACTGACAGGCTTTCTGTGTGTTGTCAAGAAAGATAGTAAAGTGTGATA 2940

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Qy 3241 CAAGCAATTTAATGAAGTAGGTTCCAGTACTAATGAAGTGGCTCCAGTATTAATGAAA 3300  
Db 3241 CAAGCAATTTAATGAAGTAGGTTCCAGTACTAATGAAGTGGCTCCAGTATTAATGAAA 3300  
Qy 3301 TAGGTTCCAGTGAAGAAACATTCAGAGCAACTAGTGAAGAAACAGAGGGCAAAATTGA 3360  
Db 3301 TAGGTTCCAGTGAAGAAACATTCAGAGCAACTAGTGAAGAAACAGAGGGCAAAATTGA 3360  
Qy 3361 ATGCTATGCTTAGATTAAGGGTTTTGCAACCTGAGGCTATTAACAAAGTCTCTCGAA 3420  
Db 3361 ATGCTATGCTTAGATTAAGGGTTTTGCAACCTGAGGCTATTAACAAAGTCTCTCGAA 3420  
Qy 3421 GTAATTTGAACATCTGAAATTAAGAAAGCAAGAAATGAAGAGTGTCAAGTCTTTA 3480  
Db 3421 GTAATTTGAACATCTGAAATTAAGAAAGCAAGAAATGAAGAGTGTCAAGTCTTTA 3480  
Qy 3481 ATACAGATTTCTCCATATCTGATTCAGATTAAGTAAAGTGAAGTGAAGTGAAGTATGC 3540  
Db 3481 ATACAGATTTCTCCATATCTGATTCAGATTAAGTAAAGTGAAGTGAAGTGAAGTATGC 3540  
Qy 3541 ATGCATCTCAGGTTTTGTTCTGAGACACCTGATGACCTGTTAGATGATGTTGAATTAAG 3600  
Db 3541 ATGCATCTCAGGTTTTGTTCTGAGACACCTGATGACCTGTTAGATGATGTTGAATTAAG 3600  
Qy 3601 AAGATTAAGTGTGCTGAAATGACATTAAGAAAGTTCGCTGTTTTAGCAAAACCG 3660  
Db 3601 AAGATTAAGTGTGCTGAAATGACATTAAGAAAGTTCGCTGTTTTAGCAAAACCG 3660  
Qy 3661 TCCAGAGAGAGCTTAAGCAGAGTCTTACCCCTTTTACCCTTAACCAATTAAGTGGCTCAG 3720  
Db 3661 TCCAGAGAGAGCTTAAGCAGAGTCTTACCCCTTTTACCCTTAACCAATTAAGTGGCTCAG 3720  
Qy 3721 GTTACCGAAGAGGGGCCAAAGAAATTAAGAGTCTTCCAGAGAAACCTTATCTAGTGAAG 3780  
Db 3721 GTTACCGAAGAGGGGCCAAAGAAATTAAGAGTCTTCCAGAGAAACCTTATCTAGTGAAG 3780  
Qy 3781 AAGAGCTTCCCTGCTTCCAAACATTTGTTTGTAAAGTAAACATTAATACCTTCTCAGT 3840  
Db 3781 AAGAGCTTCCCTGCTTCCAAACATTTGTTTGTAAAGTAAACATTAATACCTTCTCAGT 3840  
Qy 3841 CTACTAGGCAATGACACCTGTTCTACCGAGTGTCTGTCTAAGAAACACAGAGAAATTAAT 3900  
Db 3841 CTACTAGGCAATGACACCTGTTCTACCGAGTGTCTGTCTAAGAAACACAGAGAAATTAAT 3900  
Qy 3901 TATCATTAAGAAATAGCTTAATGATCTGACAGTAACAGAGTAATTTGCAAGGATCTC 3960  
Db 3901 TATCATTAAGAAATAGCTTAATGATCTGACAGTAACAGAGTAATTTGCAAGGATCTC 3960  
Qy 3961 AGGAACATCACTTAAGTGAAGAAACAAATGTTCTGCTAGCTGTTTTCTTCAAGTCA 4020  
Db 3961 AGGAACATCACTTAAGTGAAGAAACAAATGTTCTGCTAGCTGTTTTCTTCAAGTCA 4020

OY	4021	TTGAAATTGGAAAGACTTGAATCTGAAATATACAAACACCAGAAATCCCTTCTGTGAATGGTCTT	4080
Db	4021	GTGAATTGGAAAGACTTGAATCTGAAATATACAAACACCAGAAATCCCTTCTGTGAATGGTCTT	4080
OY	4081	CCAAACAATGAGGATCATGATCTGAAAGCAGAGGAGTGGTCTGAGTACAGAAATTTGG	4140
Db	4081	CCAAACAATGAGGATCATGATCTGAAAGCAGAGGAGTGGTCTGAGTACAGAAATTTGG	4140
OY	4141	TTTCAGATGATGAAGAAAGGAAACGGGCTTTGGAAGAAATATCAAGAAAGCAAAACA	4200
Db	4141	TTTCAGATGATGAAGAAAGGAAACGGGCTTTGGAAGAAATATCAAGAAAGCAAAACA	4200
OY	4201	TGGATTCAAACTTAAAGTGAAGAGATCTGGGTGTGAAGATGAACAGCGTCTTGAAG	4260
Db	4201	TGGATTCAAACTTAAAGTGAAGAGATCTGGGTGTGAAGATGAACAGCGTCTTGAAG	4260
OY	4261	ACTGCTCAGGGCTATCTCTCAGATGTAATTTTAAACACTCAGAGAGGATACATACG	4320
Db	4261	ACTGCTCAGGGCTATCTCTCAGATGTAATTTTAAACACTCAGAGAGGATACATACG	4320
OY	4321	AACATTAACCTGATTAAGTCTCCAGCAGAAATGGCTTAACTAAGACTGTGTAGAACACG	4380
Db	4321	AACATTAACCTGATTAAGTCTCCAGCAGAAATGGCTTAACTAAGACTGTGTAGAACACG	4380
OY	4381	ATGGAGGCCAGGCTTCTTAAACAGCTACCTTCCATATAAGATGATCTCTGCTGCTTGAAG	4440
Db	4381	ATGGAGGCCAGGCTTCTTAAACAGCTACCTTCCATATAAGATGATCTCTGCTGCTTGAAG	4440
OY	4441	ACCTCGCAAAATCCAGAACAAAGCATCATGAAAGAAAGCAGATATTAATCTTCAAGAAAGTA	4500
Db	4441	ACCTCGCAAAATCCAGAACAAAGCATCATGAAAGAAAGCAGATATTAATCTTCAAGAAAGTA	4500
OY	4501	GTGAATACCTATTAAGCCAGAAATCCAGAAAGCCTTTTCTGTGACAAAGTTTGAAGTCTG	4560
Db	4501	GTGAATACCTATTAAGCCAGAAATCCAGAAAGCCTTTTCTGTGACAAAGTTTGAAGTCTG	4560
OY	4561	GAGATAGTTCCTACGATTAAGAAATTAAGAAACCAAGAGTGAAGAAAGTCAATCCCTTTAAAT	4620
Db	4561	GAGATAGTTCCTACGATTAAGAAATTAAGAAACCAAGAGTGAAGAAAGTCAATCCCTTTAAAT	4620
OY	4621	GCCCATCATTAAGATATGATAGTGTGTATGACAGTGTGCTGTGGAGTCTTCAGAAATAAAG	4680
Db	4621	GCCCATCATTAAGATATGATAGTGTGTATGACAGTGTGCTGTGGAGTCTTCAGAAATAAAG	4680
OY	4681	ACTACCAATCTCCAGAGAGGCTCATTTAAGTGTGTATGATGTGAGAGCAACGCTGGAG	4740
Db	4681	ACTACCAATCTCCAGAGAGGCTCATTTAAGTGTGTATGATGTGAGAGCAACGCTGGAG	4740
OY	4741	AGTCTGGGACACACATTTTACGGAAACATCTTATCTTGCCAAAGCAATCTTAGAGGGAA	4800
Db	4741	AGTCTGGGACACACATTTTACGGAAACATCTTATCTTGCCAAAGCAATCTTAGAGGGAA	4800
OY	4801	CCCCCTTACCTGGAATCTGGAATCAGCCCTTCTCGATGAGCCCTGAATCTGATCTCTTG	4860
Db	4801	CCCCCTTACCTGGAATCTGGAATCAGCCCTTCTCGATGAGCCCTGAATCTGATCTCTTG	4860
OY	4861	AAGACAGAGCCCCAGAGTCAAGTCTGTGTGCAACATACATCTTCAACTCTGATCTTGA	4920
Db	4861	AAGACAGAGCCCCAGAGTCAAGTCTGTGTGCAACATACATCTTCAACTCTGATCTTGA	4920
OY	4921	AAAGTTCACCAATTTGAAGTGTGCAATCTGCCAGAGGTTCAGCTGTCTCTACTACTACTG	4980
Db	4921	AAAGTTCACCAATTTGAAGTGTGCAATCTGCCAGAGGTTCAGCTGTCTCTACTACTACTG	4980
OY	4981	ATACTGCTGGGATATATGCAATGGAAGAAAGTGTAGAGAGGAGAGCAAGAAATTTGACAG	5040
Db	4981	ATACTGCTGGGATATATGCAATGGAAGAAAGTGTAGAGAGGAGAGCAAGAAATTTGACAG	5040
OY	5041	CTTCAACAGAAAGGCTCAACAAAGAAATGTCCATGATGTGTCTGAGTCCACCCAGAG	5100
Db	5041	CTTCAACAGAAAGGCTCAACAAAGAAATGTCCATGATGTGTCTGAGTCCACCCAGAG	5100
OY	5101	AATTTATGCTGTATCAAGATTGTGCAGAAACACCAATCATCTTTAATCTAATTAATTA	5160

Db	5101	AAATTATGCTGTGTGACAGTTTGCAGAAACCCACATCATCTTAATCTTAATTTA	5160
QY	5161	CTGAAGAGACTACTCATGTGTGTTATGAAAACAGATGCTGAAGTTGTGTGAAACGAC	5220
Db	5161	CTGAAGAGACTACTCATGTTGTTATGAAAACAGATGCTGAAGTTGTGTGAAACGAC	5220
QY	5221	TGAATATTTTCTAGGAATTCGGGAGAGAAATGGGTAAGTTAGCTATTTCTGGGTGACC	5280
Db	5221	TGAATATTTTCTAGGAATTCGGGAGAGAAATGGGTAAGTTAGCTATTTCTGGGTGACC	5280
QY	5281	AGCTATTAAGAAAGAAAATGCTGATGATGCAATTTTGAAGTCAAGAGAGATGG	5340
Db	5281	AGCTATTAAGAAAGAAAATGCTGATGATGCAATTTTGAAGTCAAGAGAGATGG	5340
QY	5341	TCAATGGAAGAAACCAACAGAGTCCAAAGCAGACAGAGATCCACAGACAGAAAGTCT	5400
Db	5341	TCAATGGAAGAAACCAACAGAGTCCAAAGCAGACAGAGATCCACAGACAGAAAGTCT	5400
QY	5401	TCAGGGGGCTAGAAATCTGTGCTATGAGGCCCTTTCACCAATGCCACAGATCAACTGG	5460
Db	5401	TCAGGGGGCTAGAAATCTGTGCTATGAGGCCCTTTCACCAATGCCACAGATCAACTGG	5460
QY	5461	AATGATGCTTCACTGTGTGGTCTTCTGTGTGAGAGAGCTTTCATCATCACTCTG	5520
Db	5461	AATGATGCTTCACTGTGTGGTCTTCTGTGTGAGAGAGCTTTCATCATCACTCTG	5520
QY	5521	GCACAGGTGTCAACCCCAATTTGTTGTGACAGCAGATGCTGTGACAGAGACATGGCT	5580
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QY	5581	TCATATGCAATTTGGGCAATGTGTAGAGCACTGTGTGACCCGAGAGTGGGTGTTGAC	5640
Db	5581	TCATATGCAATTTGGGCAATGTGTAGAGCACTGTGTGACCCGAGAGTGGGTGTTGAC	5640
QY	5641	GTTAGACACTTACAGAGTCCAGAGAGCTGACACCTTACCTGATATCCCAAGTCCGCCA	5700
Db	5641	GTTAGACACTTACAGAGTCCAGAGAGCTGACACCTTACCTGATATCCCAAGTCCGCCA	5700
QY	5701	GCCACTACTGA 5711	
Db	5701	GCCACTACTGA 5711	

RESULT 2  
 US-09-982-828-1  
 ; Sequence 1, Application US/09982828  
 ; Publication No. US20030022184A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Murphy, Patricia D.  
 ; Allen, Antoinette C.  
 ; Alvares, Christopher P.  
 ; Critz, Brenda S.  
 ; Olson, Sheri J.  
 ; Thunder, Denise  
 ; Zeng, Bin  
 ; TITLE OF INVENTION: Coding Sequences of the Human  
 ; BRCA1 Gene  
 ; NUMBER OF SEQUENCES: 72  
 ; CORRESPONDENCE ADDRESS:  
 ; ADDRESSEE: Morgan Lewis & Bockius LLP  
 ; STREET: 1111 Pennsylvania Avenue N. W.  
 ; CITY: Washington  
 ; STATE: DC  
 ; COUNTRY: USA  
 ; ZIP: 20004  
 ; COMPUTER READABLE FORM:  
 ; MEDIUM TYPE: Floppy disk  
 ; COMPUTER: IBM PC compatible  
 ; OPERATING SYSTEM: PC-DOS/MS-DOS  
 ; SOFTWARE: PatentIn Release #1.0, Version #1.30  
 ; CURRENT APPLICATION DATA:  
 ; APPLICATION NUMBER: US/09/982.828

FILING DATE: 22-Oct-2001  
CLASSIFICATION: <Unknown>  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 09/074,453  
FILING DATE: 1998-05-06  
APPLICATION NUMBER: US 08/798,691  
FILING DATE: 1997-02-12  
APPLICATION NUMBER: US 08/598,591  
FILING DATE: 1996-02-12  
ATTORNEY/AGENT INFORMATION:  
NAME: Michael S. Tuscan  
REGISTRATION NUMBER: 43,210  
REFERENCE/DOCKET NUMBER: 44921-5053-01-US  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 202-739-3000  
TELEFAX: 202-739-3001  
INFORMATION FOR SEQ ID NO: 1:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 5711 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: not relevant  
TOPOLOGY: linear  
MOLECULE TYPE: cDNA  
ORIGINAL SOURCE:  
ORGANISM: Homo sapiens  
STRAIN: BRCAL (om11)  
POSITION IN GENOME:  
CHROMOSOME/SEGMENT: 17  
MAP POSITION: 17q21  
SEQUENCE DESCRIPTION: SEQ ID NO: 1:  
US-09-982-828-1

Query Match 100.0%; Score 5711; DB 11; Length 5711;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 5711; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AGCTCGAGAGACTTCTGTGAGACCCCGCACAAGGCTGTGGGGTTTCTCATTAATCTGGGCC 60  
DB 1 AGCTCGAGAGACTTCTGTGAGACCCCGCACAAGGCTGTGGGGTTTCTCATTAATCTGGGCC 60

QY 61 CTTGCGCTCAGAGAGGCTTCAACCCCTCTGCTGTGTAAGTTCAATGGAAAGAA 120  
DB 61 CTTGCGCTCAGAGAGGCTTCAACCCCTCTGCTGTGTAAGTTCAATGGAAAGAA 120

QY 121 TGAATTTATCTGCTCTTGGCGTTGAAGAATGCAAAATGCTAATATGCAAGAAA 180  
DB 121 TGAATTTATCTGCTCTTGGCGTTGAAGAATGCAAAATGCTAATATGCAAGAAA 180

QY 181 TCTTAGAGTGTCCATCTGTCTGAGTGTATCAAGAACTGTCTCCCAAAAGTGTGACC 240  
DB 181 TCTTAGAGTGTCCATCTGTCTGAGTGTATCAAGAACTGTCTCCCAAAAGTGTGACC 240

QY 241 ACATATTTTGGCAAAATTTTGCATGCTGAACCTTCTCAACAGAAAGAAAGGCTTCAAGT 300  
DB 241 ACATATTTTGGCAAAATTTTGCATGCTGAACCTTCTCAACAGAAAGAAAGGCTTCAAGT 300

QY 301 GTCTTTATGTAGAATATATTAACCAAAAGAGGCTTCAAGAAAGTACGAGATTAGTTC 360  
DB 301 GTCTTTATGTAGAATATATTAACCAAAAGAGGCTTCAAGAAAGTACGAGATTAGTTC 360

QY 361 AACTTTGTAGAGATATTAAGAAATCAATTTGTGCTTCAAGTTTGAAGT 420  
DB 361 AACTTTGTAGAGATATTAAGAAATCAATTTGTGCTTCAAGTTTGAAGT 420

QY 421 ATGCAAAAGCTATATTTTGCAGAAAAGAAATTAATCTCTCAAGATCTAAAGATG 480  
DB 421 ATGCAAAAGCTATATTTTGCAGAAAAGAAATTAATCTCTCAAGATCTAAAGATG 480

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DB 541 AACCGAAATTCCTTCTTGCAAGAAACCAATCTCAAGTGTCAACTCTCTAAGCTTGAAG 600

QY 601 CTGTGAGACTCTGTAGAGCAAAAGCGGAGATCAACCTCAAAAGAGCTGTCTACATTTG 660  
DB 601 CTGTGAGACTCTGTAGAGCAAAAGCGGAGATCAACCTCAAAAGAGCTGTCTACATTTG 660

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QY 721 ATCAAGAAATTTGTAACAATCAACCCCTCAAGAACAGGAGATGAATCAGTTTGGATTCG 780  
DB 721 ATCAAGAAATTTGTAACAATCAACCCCTCAAGAACAGGAGATGAATCAGTTTGGATTCG 780

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DB 781 CAAAAAGGCTGCTTGTGAATTTTCTGAGACGATGTAAACAATCTGAACATCATCAAC 840

QY 841 CCAGTAATTAATGATTGTAACCACTGAGAGCGTGCAGCTGAGAGGATCCAGAAAGT 900  
DB 841 CCAGTAATTAATGATTGTAACCACTGAGAGCGTGCAGCTGAGAGGATCCAGAAAGT 900

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DB 901 ATCAAGGATGTTCTGTTTCAAACTTGCATGTGAGCCATGTGGCAAAATCTCATGCCA 960

QY 961 GCTCATTAACAGCATGAGAACGAGTTTACTACTTAAGACAGAAATGAATGTAGAA 1020  
DB 961 GCTCATTAACAGCATGAGAACGAGTTTACTACTTAAGACAGAAATGAATGTAGAA 1020

QY 1021 AGGCTGAATTTCTGTATTAAGCAAAACGCTGTGTTAGCAAGAGCCAAATACAT 1080  
DB 1021 AGGCTGAATTTCTGTATTAAGCAAAACGCTGTGTTAGCAAGAGCCAAATACAT 1080

QY 1081 GGGCTGGAAGTAAAGAAACATGTATGTATAGGCGGACTCCAGCACAGAAAAAGTAG 1140  
DB 1081 GGGCTGGAAGTAAAGAAACATGTATGTATAGGCGGACTCCAGCACAGAAAAAGTAG 1140

QY 1141 ATCTGAATCTGATCCCTGTGTGAGAGAAAAAGATGAATTAAGCAAACTGCATGCT 1200  
DB 1141 ATCTGAATCTGATCCCTGTGTGAGAGAAAAAGATGAATTAAGCAAACTGCATGCT 1200

QY 1201 CAGAGATCTTAGAGATCTGAAGATGTTCTTGATTAACCTAAATGACAGCATTCGA 1260  
DB 1201 CAGAGATCTTAGAGATCTGAAGATGTTCTTGATTAACCTAAATGACAGCATTCGA 1260

QY 1261 AAGTTAATGAGTGGTTTCCAGAGTGAAGTAACTGTTAGGTTTGATGACTCAATGATG 1320  
DB 1261 AAGTTAATGAGTGGTTTCCAGAGTGAAGTAACTGTTAGGTTTGATGACTCAATGATG 1320

QY 1321 GGGAGCTGAATCAAAATGCCAAAGTAGTGTATTTGAGAGTTCTAAATGAGGTAGATG 1380  
DB 1321 GGGAGCTGAATCAAAATGCCAAAGTAGTGTATTTGAGAGTTCTAAATGAGGTAGATG 1380

QY 1381 AATATTTCTGTTCTTCAAGAAAAATAGCTTAGCGCAGATGATCTCATAGGCTTTAA 1440  
DB 1381 AATATTTCTGTTCTTCAAGAAAAATAGCTTAGCGCAGATGATCTCATAGGCTTTAA 1440

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DB 1441 TATGTAAAGTGAAGAGTTCACTCCAAATAGTAGAGATATTTGAAGCAAAATAT 1500

QY 1501 TTGGAAAACTATCTGAGAAAGGCAAGCTTCCCAACTTAAGGCATGTAACGAAAAATC 1560  
DB 1501 TTGGAAAACTATCTGAGAAAGGCAAGCTTCCCAACTTAAGGCATGTAACGAAAAATC 1560

QY 1561 TAAATTAAGAGCAATTTGTAAGTGAAGCAAGATTAATCAAGAGCTTCCCAAAAT 1620  
DB 1561 TAAATTAAGAGCAATTTGTAAGTGAAGCAAGATTAATCAAGAGCTTCCCAAAAT 1620

QY 1621 AATTAAAGCTTAAAGAGCACTATCAGGCTTCACTCGAGAGATTTTATCAAGAAAG 1680

D	b	1621	AATTAAGCGTAAAGAGACCTACATCAGCGCTTCATCTGTGAGATTTTATCAAGAAAG	1680
Q	y	1681	CAGATTTGGCAGTTCAAAAAGACTCTGAAATGATTAATCAAGGAACTTAACCAAGGAGC	1740
D	b	1681	CAGATTTGGCAGTTCAAAAAGACTCTGAAATGATTAATCAAGGAACTTAACCAAGGAGC	1740
Q	y	1741	AGAATGCTCAAGTGAATGATTTACTTAATAGTGTCAATGAGATTAATAAAGGAGGAT	1800
D	b	1741	AGAATGCTCAAGTGAATGATTTACTTAATAGTGTCAATGAGATTAATAAAGGAGGAT	1800
Q	y	1801	CTAATCAGATGAGAAAAATCTTAACCAATGAAATCACTGCAAAAAAGATCTGTTTCA	1860
D	b	1801	CTAATCAGATGAGAAAAATCTTAACCAATGAAATCACTGCAAAAAAGATCTGTTTCA	1860
Q	y	1861	AAAGCAAGCTGAACCTTAAGCAGCAGTATAGAAATAGGAATTCGAATTAATTAATCC	1920
D	b	1861	AAAGCAAGCTGAACCTTAAGCAGCAGTATAGAAATAGGAATTCGAATTAATTAATCC	1920
Q	y	1921	ACAATTTCAAAAGCAGCTTAATAAGATAGGCTGAGAGGAGAGTCTTAACAGGCAATATTC	1980
D	b	1921	ACAATTTCAAAAGCAGCTTAATAAGATAGGCTGAGAGGAGAGTCTTAACAGGCAATATTC	1980
Q	y	1981	ATGCGCTTGAACCTAGTACGTAGTAAGAAATCTAAGCCCACTTAATTTGATCTGAATTCGAAA	2040
D	b	1981	ATGCGCTTGAACCTAGTACGTAGTAAGAAATCTAAGCCCACTTAATTTGATCTGAATTCGAAA	2040
Q	y	2041	TTGATAGTTGTTCTGACAGTGAAGATTAAGAAAAAGTGAACCAATTCGACGCA	2100
D	b	2041	TTGATAGTTGTTCTGACAGTGAAGATTAAGAAAAAGTGAACCAATTCGACGCA	2100
Q	y	2101	GGCAGAGCAAAACCTTAACATCATGGAAGTAAAGAACTGCACTGAGCCAGAGAAAGA	2160
D	b	2101	GGCAGAGCAAAACCTTAACATCATGGAAGTAAAGAACTGCACTGAGCCAGAGAAAGA	2160
Q	y	2161	GTAACAGCCAAATGACAGACAGTAATAAGCATGACAGTATACCTTCCAGAGCTGA	2220
D	b	2161	GTAACAGCCAAATGACAGACAGTAATAAGCATGACAGTATACCTTCCAGAGCTGA	2220
Q	y	2221	AGTTAACAAATGACAGTGTCTTTTCTTAAGTGTTCAAATACCGATTAAGTAAGAT	2280
D	b	2221	AGTTAACAAATGACAGTGTCTTTTCTTAAGTGTTCAAATACCGATTAAGTAAGAT	2280
Q	y	2281	TTGTCAATCTAGCTTCAAGAGAGAAAGAAAGAACTAAGAAACAGTTAAAGTGT	2340
D	b	2281	TTGTCAATCTAGCTTCAAGAGAGAAAGAAAGAAAGAACTAAGAAACAGTTAAAGTGT	2340
Q	y	2341	CTAATTAATGCTGAGAGACCCCAAGATCTCATGTTTAAGTGAAGAAAGGTTTGCAGCTG	2400
D	b	2341	CTAATTAATGCTGAGAGACCCCAAGATCTCATGTTTAAGTGAAGAAAGGTTTGCAGCTG	2400
Q	y	2401	AAAGATCTGTAGAGAGTGAAGTATTCAGTGTGCTGCTGATTAATGAGCACTCAGG	2460
D	b	2401	AAAGATCTGTAGAGAGTGAAGTATTCAGTGTGCTGCTGATTAATGAGCACTCAGG	2460
Q	y	2461	AAAGATCTGTAGAGTGAAGTATTCAGTGTGCTGCTGATTAATGAGCACTCAGG	2520
D	b	2461	AAAGATCTGTAGAGTGAAGTATTCAGTGTGCTGCTGATTAATGAGCACTCAGG	2520
Q	y	2521	GTGTGAGTCAAGTGTGCAACATTTGAAAAAGGAGGCTAATTCATGTTGTTTCAAG	2580
D	b	2521	GTGTGAGTCAAGTGTGCAACATTTGAAAAAGGAGGCTAATTCATGTTGTTTCAAG	2580
Q	y	2581	ATAATAGAAATGACAGAAAGCTTAACTGATTCCTGAGGAGTAAATTCACCAATTC	2640
D	b	2581	ATAATAGAAATGACAGAAAGCTTAACTGATTCCTGAGGAGTAAATTCACCAATTC	2640
Q	y	2641	GGGAAACAGAGATGAAATGAGAAAGTGAACCTGATGCTCAGATTTGGCAGATTAAT	2700
D	b	2641	GGGAAACAGAGATGAAATGAGAAAGTGAACCTGATGCTCAGATTTGGCAGATTAAT	2700
Q	y	2701	TCAGAGTTTCAAGGCGCAGTCAATTTGCTGTTTTCAAATCCAGAAATGCAAGAGG	2760
D	b	2701	TCAGAGTTTCAAGGCGCAGTCAATTTGCTGTTTTCAAATCCAGAAATGCAAGAGG	2760

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Q	y	2761	AATGNGCAACATTTCTGCGCCGACCTGCGGCTCCTTAAGAAACAAAGTCCAAAGCACTT	2820
D	b	2761	AATGNGCAACATTTCTGCGCCGACCTGCGGCTCCTTAAGAAACAAAGTCCAAAGCACTT	2820
Q	y	2821	TTGAATGTGAACAAAGAGGAAAGAAATCAAGGAAAGAAATGAGTCTAATATCAAGCTGTAC	2880
D	b	2821	TTGAATGTGAACAAAGAGGAAAGAAATCAAGGAAAGAAATGAGTCTAATATCAAGCTGTAC	2880
Q	y	2881	AGACATTAATATCACTGACAGGCTTCTGTTGTTGGTCAAGAAAGATTAAGCAAGTTGATA	2940
D	b	2881	AGACATTAATATCACTGACAGGCTTCTGTTGTTGGTCAAGAAAGATTAAGCAAGTTGATA	2940
Q	y	2941	ATGCGCAATGTATATCAAGAGGCTCAGTGTTCATCACTCAGTTTCAGAGGCA	3000
D	b	2941	ATGCGCAATGTATATCAAGAGGCTCAGTGTTCATCACTCAGTTTCAGAGGCA	3000
Q	y	3001	ACGAACTGACCTCATTAACCTCAATTAACATGACCTTTTCAAAAACCATATGCTATAC	3060
D	b	3001	ACGAACTGACCTCATTAACCTCAATTAACATGACCTTTTCAAAAACCATATGCTATAC	3060
Q	y	3061	CACCACTTTTCCATCAAGTCAATTTGTTAAACTAAATGTAAGAAAAATCTGCTAGAGG	3120
D	b	3061	CACCACTTTTCCATCAAGTCAATTTGTTAAACTAAATGTAAGAAAAATCTGCTAGAGG	3120
Q	y	3121	AAAATTTGAGGAACTTCAATGTCACCTGAAAGAGAAATGGGAAATGAGAACTTCCAA	3180
D	b	3121	AAAATTTGAGGAACTTCAATGTCACCTGAAAGAGAAATGGGAAATGAGAACTTCCAA	3180
Q	y	3181	GTAACAGTACGACATTAAGCCGTATTAACATTAAGAAAGAAATGTTTTTAAAGAGCAGCT	3240
D	b	3181	GTAACAGTACGACATTAAGCCGTATTAACATTAAGAAAGAAATGTTTTTAAAGAGCAGCT	3240
Q	y	3241	CAAGCAATTAATTAAGAGTACGTTCCAGTCTAATGAAAGTGGCTCCAGTATTAATGAAA	3300
D	b	3241	CAAGCAATTAATTAAGAGTACGTTCCAGTCTAATGAAAGTGGCTCCAGTATTAATGAAA	3300
Q	y	3301	TAGGTTCCAGATGAGAAACCACTCAAGAGAACTAAGTGAAGAAAGAGGAGGCAAAATTTGA	3360
D	b	3301	TAGGTTCCAGATGAGAAACCACTCAAGAGAACTAAGTGAAGAAAGAGGAGGCAAAATTTGA	3360
Q	y	3361	ATGCTATGCTTAGATTTAGGGGTTTGGCACTGAGGCTATTAACAAAGTCTTCCTGAAA	3420
D	b	3361	ATGCTATGCTTAGATTTAGGGGTTTGGCACTGAGGCTATTAACAAAGTCTTCCTGAAA	3420
Q	y	3421	GTAATTTGAACATTCGAAATTAATAAGCAAGAAATTAAGAAAGTACGACTGTA	3480
D	b	3421	GTAATTTGAACATTCGAAATTAATAAGCAAGAAATTAAGAAAGTACGACTGTA	3480
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D	b	3481	ATAAGATTTCTCCATATCTGATTCAGATTAAGAAAGAGCTAATGGAGTATGTC	3540
Q	y	3541	ATGCAATCTCAGATTTGTTCTGAGACACCTGATGACCTGTTAGATGATGAGTAAAGG	3600
D	b	3541	ATGCAATCTCAGATTTGTTCTGAGACACCTGATGACCTGTTAGATGATGAGTAAAGG	3600
Q	y	3601	AAAGTACTAGTTTGGCTGAGAAATGACATTAAGGAAAGTTCGCTGTTTTCAGCAAAAGCG	3660
D	b	3601	AAAGTACTAGTTTGGCTGAGAAATGACATTAAGGAAAGTTCGCTGTTTTCAGCAAAAGCG	3660
Q	y	3661	TCCAGAGAGGAGCTTACGAGAGGCTCCTAGCCCTTTCACCCATACCATTTGGCTCAGG	3720
D	b	3661	TCCAGAGAGGAGCTTACGAGAGGCTCCTAGCCCTTTCACCCATACCATTTGGCTCAGG	3720
Q	y	3721	GTTACCGAAGAGGGGCAAGAAATTAAGATCTCAGAGAGAACTTATCTAGTGAAGATG	3780
D	b	3721	GTTACCGAAGAGGGGCAAGAAATTAAGATCTCAGAGAGAACTTATCTAGTGAAGATG	3780
Q	y	3781	AAGAGCTTCCCTGCTTCCAAACATTTGTTTGTGTAAGTAACATATACCTTCTCAGT	3840
D	b	3781	AAGAGCTTCCCTGCTTCCAAACATTTGTTTGTGTAAGTAACATATACCTTCTCAGT	3840

QY 3841 CTACAGCATAGACACCGTCTGCTACGAGTGTCTGTAAAGACACAGAGGAAATTTAT 3900  
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 Db 3841 CTACTAGGCATAGACCCGTTGCTACCGAGTGTCTGTAAAGACACAGAGGAAATTTAT 3900  
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 QY 3901 TATCATTTAGAGATAGCTTAAATGACCTGACGTACCAAGTAAATTTGGCAAGGATCTC 3960  
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 Db 3901 TATCATTTAGAGATAGCTTAAATGACCTGACGTACCAAGTAAATTTGGCAAGGATCTC 3960  
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 QY 3961 AGGAACATCACTTGTGTAGAGAAACAAAATGTTCTGTAGCTTTTCTTCAAGTGA 4020  
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 Db 3961 AGGAACATCACTTGTGTAGAGAAACAAAATGTTCTGTAGCTTTTCTTCAAGTGA 4020  
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 Db 4021 GTGAATTTGAAAGACTTGAAGTGAACCAACCAAGATCTTCTTGAATTTGTTCTT 4080  
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 Db 4081 CCAACCAATGAGGATGATGAGTGAAGCCAGAGAGTGTGTGAGTGAACAGAAATGG 4140  
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 Db 4261 ACTGCTCAGAGGCTATCTCTCAGAGTGAATTTTAAACACTCAGAGAGAGGATACATGC 4320  
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 Db 4381 ATGGAGGACAGCTCTAAACAGCTAACCCCTGCATATAAGTACCTCTGCTGAGG 4440  
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 QY 4441 ACCTCGGAATCCAGAACCAAGCAGATCAGAAAAGAGATTTAACTTCAAGAAAAGTA 4500  
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 Db 4441 ACCTCGGAATCCAGAACCAAGCAGATCAGAAAAGAGATTTAACTTCAAGAAAAGTA 4500  
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 Db 4501 GTGAATCCCTTAATAGCCAGAAATCCAGAAAGGCTTTCTGCTGACAAAGTTGAGTGTG 4560  
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 Db 5101 AATTTATCTGTGTATAGAGTTTGGCAGAAAAACACACATCACTTTAACTTAATTA 5160  
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 Db 5161 CTGAAGAGACTATCTATGTTGTTATGAGAAACAGATGCTGAGTGTGTGTGAGAGAGCAG 5220  
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 Db 5221 TGAATATTTTCTAGAAATTTGGGAGGAGAAATGGGTAGTTAGTATTTCTGGTGAACCC 5280  
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 QY 5281 AGCTATTAAAGAAAGAAATGCTGAATGAGCATGATTTTGAAGTCAAGAGAGATGTGG 5340  
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 Db 5281 AGCTATTAAAGAAAGAAATGCTGAATGAGCATGATTTTGAAGTCAAGAGAGATGTGG 5340  
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 QY 5341 TCAATGAGAAAGAACCAAGGCTCCAAAGCCAGAGCAAGAGATCCAGAGCAGAAAGATCT 5400  
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 Db 5341 TCAATGAGAAAGAACCAAGGCTCCAAAGCCAGAGCAAGAGATCCAGAGCAGAAAGATCT 5400  
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 QY 5401 TCAGGGGCTGAATCTGTTGCTATGTGGGCTTACCAACAATGCCACAGATCAACTGG 5460  
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 Db 5401 TCAGGGGCTGAATCTGTTGCTATGTGGGCTTACCAACAATGCCACAGATCAACTGG 5460  
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 QY 5461 AATGATGATACAGCTGTGTGTGCTGTGTGTGAGAGAGGCTTCAATTCACCTTG 5520  
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 Db 5641 GTGTAGCACTTACAGGTGCCAGAGCTGAGACACTTACTGATACCCAGATCCCCAGCA 5700  
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 QY 5701 GCCACTACTGA 5711  
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 Db 5701 GCCACTACTGA 5711  
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RESULT 3  
 US-09-734-672-5  
 ; Sequence 5, Application US/09734672  
 ; Publication No. US20020183268A1  
 GENERAL INFORMATION:  
 APPLICANT: Murphy, Patricia D.  
 ; Allen, Antoinette C.  
 ; Alvaes, Christopher P.  
 ; Critz, Brenda S.  
 ; Olson, Sheri J.  
 ; Schelter, Denise B.  
 ; Zeng, Bin  
 TITLE OF INVENTION: Coding Sequences of the Human  
 ; BRCAL Gene  
 NUMBER OF SEQUENCES: 72  
 CORRESPONDENCE ADDRESS:  
 ; ADDRESSEE: Morgan Lewis & Bockius LLP

STREET: 1111 Pennsylvania Ave., N.W.  
 CITY: Washington  
 STATE: District of Columbia  
 COUNTRY: USA  
 ZIP: 20004

COMPUTER READABLE FORM:  
 MEDIUM TYPE: Floppy disk  
 COMPUTER: IBM PC compatible  
 OPERATING SYSTEM: PC-DOS/MS-DOS  
 SOFTWARE: PatentIn Release #1.0, Version #1.30

CURRENT APPLICATION DATA:  
 APPLICATION NUMBER: US/09/734,672  
 FILING DATE: 03-Dec-2000

PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: US 08/966,436  
 FILING DATE: 07-No. US20020183268A1-97  
 APPLICATION NUMBER: US 08/598,591  
 FILING DATE: 12-Feb-96

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 TELECOMMUNICATION INFORMATION:  
 TELEPHONE: 202-739-3000  
 TELEFAX: 202-739-3001

INFORMATION FOR SEQ ID NO: 5:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 5711 base pairs  
 TYPE: nucleic acid  
 STRANDEDNESS: No. US20020183268A1 Relevant  
 TOPOLOGY: linear

MOLECULE TYPE: cDNA  
 ORIGINAL SOURCE:  
 ORGANISM: Homo sapiens  
 STRAIN: BRCA1  
 POSITION IN GENOME:  
 CHROMOSOME/SEGMENT: 17  
 MAP POSITION: 17q21  
 SEQUENCE DESCRIPTION: SEQ ID NO: 5:  
 US-09-734-672-5

Query Match 100.0%; Score 5709.4; DB 10; Length 5711;  
 Best Local Similarity 100.0%; Pred. No. 0;  
 Matches 5710; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 AGCTGCTGAGACCTCTCGGAGCCCGGACACGAGCTGTGGGTTCTCGATATCTAGGACC 60  
 DB 1 AGCTGCTGAGACCTCTCGGAGCCCGGACACGAGCTGTGGGTTCTCGATATCTAGGACC 60

QY 61 CTTGGGCTCAGGAGGCTTCACTCTGCTGTGGTAAAGTTCATTGGAAACAGAAAGAA 120  
 DB 61 CTTGGGCTCAGGAGGCTTCACTCTGCTGTGGTAAAGTTCATTGGAAACAGAAAGAA 120

QY 121 TGGATTATCTGCTCTTGGCGTTGAAGAGTCAAAAATGTCTATATGCTATGCAAAA 180  
 DB 121 TGGATTATCTGCTCTTGGCGTTGAAGAGTCAAAAATGTCTATATGCTATGCAAAA 180

QY 181 TCTTGAAGTCCATCTGTGAGTTGATCAAGAACTGTCTCCCAAAAGTGTGACC 240  
 DB 181 TCTTGAAGTCCATCTGTGAGTTGATCAAGAACTGTCTCCCAAAAGTGTGACC 240

QY 241 ACATATTTTGCATAATTTTGCATGTAACCTTCAACACAGAAAGAGGCTTCAACAGT 300  
 DB 241 ACATATTTTGCATAATTTTGCATGTAACCTTCAACACAGAAAGAGGCTTCAACAGT 300

QY 301 GTCTTTATGTAGATGATATATACCAAAAGAGGCTTCAACAGAAAGTACGAGATTAGTC 360  
 DB 301 GTCTTTATGTAGATGATATATACCAAAAGAGGCTTCAACAGAAAGTACGAGATTAGTC 360

QY 361 AACTGTTGAAGAGCTATATGAAATCATTTGCTTTTCAAGTTACACAGATTGGAGT 420  
 DB 361 AACTGTTGAAGAGCTATATGAAATCATTTGCTTTTCAAGTTACACAGATTGGAGT 420

QY 421 ATGCAAGACGTATATTTTGCATAAAAGAAATATATCTCTCGATGACATCTAAAGATG 480  
 DB 421 ATGCAAGACGTATATTTTGCATAAAAGAAATATATCTCTCGATGACATCTAAAGATG 480

QY 481 AAGTTCTATCATCCAAAGTATGGCTTCAAGAAACCGTCCAAAGACTTCTACAGAGTG 540  
 DB 481 AAGTTCTATCATCCAAAGTATGGCTTCAAGAAACCGTCCAAAGACTTCTACAGAGTG 540

QY 541 AACCCGAAATCTCTTCTTGAAGGAAACAGCTCAGTGTCCAACTCTTAACCTTGA 600  
 DB 541 AACCCGAAATCTCTTCTTGAAGGAAACAGCTCAGTGTCCAACTCTTAACCTTGA 600

QY 601 CTGTGAGAACTCTGAGCAAAAGCAGCGGATACAACTCAAAAGACGTCTGTCTACATG 660  
 DB 601 CTGTGAGAACTCTGAGCAAAAGCAGCGGATACAACTCAAAAGACGTCTGTCTACATG 660

QY 661 AATTGGATCTGATTTCTTGAAGTATACCGTTTATATAGGCAACTTATGCAAGTGGAG 720  
 DB 661 AATTGGATCTGATTTCTTGAAGTATACCGTTTATATAGGCAACTTATGCAAGTGGAG 720

QY 721 ATCAAGATTGTTCAAAATCAACCCCTCAAGGAAACAGGATGAATCAGTTGATTCG 780  
 DB 721 ATCAAGATTGTTCAAAATCAACCCCTCAAGGAAACAGGATGAATCAGTTGATTCG 780

QY 781 CAAAAAGGCTGCTTGTGAATTTTCTGAGACGATGTAACTGAACATCATCAAC 840  
 DB 781 CAAAAAGGCTGCTTGTGAATTTTCTGAGACGATGTAACTGAACATCATCAAC 840

QY 841 CCAATTATATGATTTGAAACCACTGGAAGCGTGTGCAAGAGGATCCAGAAAAGT 900  
 DB 841 CCAATTATATGATTTGAAACCACTGGAAGCGTGTGCAAGAGGATCCAGAAAAGT 900

QY 901 ATCAAGGATGTTCTGTTCAAACTTGATGAGGACATGTTGGCACAATATCTGACCA 960  
 DB 901 ATCAAGGATGTTCTGTTCAAACTTGATGAGGACATGTTGGCACAATATCTGACCA 960

QY 961 GCTCATTAACAGATGAGAAAGCAAGTTATTACTCATTAAGACAGATGATAGAAA 1020  
 DB 961 GCTCATTAACAGATGAGAAAGCAAGTTATTACTCATTAAGACAGATGATAGAAA 1020

QY 1021 AGGCTGAATTTCTGTAATTAAGCAAAACGCTGTGTTAGCAAGGACCAATACAT 1080  
 DB 1021 AGGCTGAATTTCTGTAATTAAGCAAAACGCTGTGTTAGCAAGGACCAATACAT 1080

QY 1081 GGGCTGGAAGTAAAGAAACATGTAATGATAGCGGACCTCCAGACAGAAAAAGGTAG 1140  
 DB 1081 GGGCTGGAAGTAAAGAAACATGTAATGATAGCGGACCTCCAGACAGAAAAAGGTAG 1140

QY 1141 ATCTGAATGCTGATCCCTGTGTGAGAGAAAAAGATGAAATAGAGAAATGCGCATGCT 1200  
 DB 1141 ATCTGAATGCTGATCCCTGTGTGAGAGAAAAAGATGAAATAGAGAAATGCGCATGCT 1200

QY 1201 CAGAGATCTTAGAGATCTGAAGTGTCTTGGATACCTAATATGCGACATTCGA 1260  
 DB 1201 CAGAGATCTTAGAGATCTGAAGTGTCTTGGATACCTAATATGCGACATTCGA 1260

QY 1261 AAGTTAATGAGTGGTTTCCAGAAAGTGAATCTGTTAGTTCGATGATCAATGATG 1320  
 DB 1261 AAGTTAATGAGTGGTTTCCAGAAAGTGAATCTGTTAGTTCGATGATCAATGATG 1320

QY 1321 GGGAGTCTGAATCAAAATGCCAAGTAGCTGATGATGGAAGTCTTAATAGGTAGATG 1380  
 DB 1321 GGGAGTCTGAATCAAAATGCCAAGTAGCTGATGATGGAAGTCTTAATAGGTAGATG 1380

QY 1381 AATATTTCTGTTCTTCAAGAGAAATAGACTTAAGTGGCAAGATCTCATAGAGCTTTAA 1440  
 DB 1381 AATATTTCTGTTCTTCAAGAGAAATAGACTTAAGTGGCAAGATCTCATAGAGCTTTAA 1440

QY 1441 TATGTAAGAGTGAAGGTTCACTCCAAATGATGAGAGATTAATGCAAAATAT 1500  
 DB 1441 TATGTAAGAGTGAAGGTTCACTCCAAATGATGAGAGATTAATGCAAAATAT 1500

QY 1501 TTGGAAAACTATCGAAGAAAGCAAGCTCCCAACTTAAGCATGTAATCTGAATATC 1560



Db 1501 TTGGAAAACTTACGGAAGAGGAGCCTCCCACTTAAGCATTACTGAATAATC 1560  
Qy 1561 TAAATTAATGAGCAATTTGTTACTGAGCCAGATATATCAAGAGGTCCCTCACAAATA 1620  
Db 1561 TAAATTAATGAGCAATTTGTTACTGAGCCAGATATATCAAGAGGTCCCTCACAAATA 1620  
Qy 1621 AATTAAGCGTAAAGAGAGAGCTCATGAGGCTTCATCTGAGGATTTTATCAAGAAAG 1680  
Db 1621 AATTAAGCGTAAAGAGAGAGCTCATGAGGCTTCATCTGAGGATTTTATCAAGAAAG 1680  
Qy 1681 CAGATTTGGCAGTTCAAAAGACTCCTGAAATGATTAATCAAGGAACTTAACCAACGAGC 1740  
Db 1681 CAGATTTGGCAGTTCAAAAGACTCCTGAAATGATTAATCAAGGAACTTAACCAACGAGC 1740  
Qy 1741 AGAATGGTCAAGTGAATTAATTAATTAAGTGGTCAATGAGATTAACCAAGGTGATT 1800  
Db 1741 AGAATGGTCAAGTGAATTAATTAATTAAGTGGTCAATGAGATTAACCAAGGTGATT 1800  
Qy 1801 CTATTCAGATGAGAAAAATCCTAACCCCAATGAAATCACTGAAAAAAGATCTGTTTCA 1860  
Db 1801 CTATTCAGATGAGAAAAATCCTAACCCCAATGAAATCACTGAAAAAAGATCTGTTTCA 1860  
Qy 1861 AAACGAAAGCTGAACCTTAAGCAGCAGTATTAAGCAATATGGAATCTCGAATTAATATCC 1920  
Db 1861 AAACGAAAGCTGAACCTTAAGCAGCAGTATTAAGCAATATGGAATCTCGAATTAATATCC 1920  
Qy 1921 ACAATTCAAAAGCAGCTTAAGAAAGAAATAGGCTGAGAGAGAAAGTCTTCAACAGCATATTC 1980  
Db 1921 ACAATTCAAAAGCAGCTTAAGAAAGAAATAGGCTGAGAGAGAAAGTCTTCAACAGCATATTC 1980  
Qy 1981 ATGGCTTGAATCTAGTACTGATGAGAAATCTTAAGCCCACTTAATTTGATCTGAATTGGCAA 2040  
Db 1981 ATGGCTTGAATCTAGTACTGATGAGAAATCTTAAGCCCACTTAATTTGATCTGAATTGGCAA 2040  
Qy 2041 TTGATAGTTGTTCTAGCAGTGAAGAGATTAAGAAAAAAGTACAAACCAAAATGCCAGTCA 2100  
Db 2041 TTGATAGTTGTTCTAGCAGTGAAGAGATTAAGAAAAAAGTACAAACCAAAATGCCAGTCA 2100  
Qy 2101 GGCAACAGAGAAACCTCAACTCATGAGAGGTAAGAACTTGCAACTGAGGCAAGAAAG 2160  
Db 2101 GGCAACAGAGAAACCTCAACTCATGAGAGGTAAGAACTTGCAACTGAGGCAAGAAAG 2160  
Qy 2161 GTAAACAGCCAAATGAAACAGACAGTAAAGACATGACAGTATCTTTCCAGAGCTGA 2220  
Db 2161 GTAAACAGCCAAATGAAACAGACAGTAAAGACATGACAGTATCTTTCCAGAGCTGA 2220  
Qy 2221 AGTTAACAAATGCACTGGTCTTTTACTTAAGTGTTCAAATPACAGTGAATTAAGAAAT 2280  
Db 2221 AGTTAACAAATGCACTGGTCTTTTACTTAAGTGTTCAAATPACAGTGAATTAAGAAAT 2280  
Qy 2281 TTGTCAATCTAGCTTCCAGAGAGAGAAAGAAAGAACTAGAAAACAGTTAAAGTGT 2340  
Db 2281 TTGTCAATCTAGCTTCCAGAGAGAGAAAGAAAGAAAGAACTAGAAAACAGTTAAAGTGT 2340  
Qy 2341 CTAATTAATGCTGAAGAGACCCCAAGATCTCATGTTAAGTGAAGAAAGGTTTTGCAACTG 2400  
Db 2341 CTAATTAATGCTGAAGAGACCCCAAGATCTCATGTTAAGTGAAGAAAGGTTTTGCAACTG 2400  
Qy 2401 AAAAGTCTGAGAGAGTGAAGTGAATTTGACTGAGTCTGGTACATTAATGAGCACTCAGG 2460  
Db 2401 AAAAGTCTGAGAGAGTGAAGTGAATTTGACTGAGTCTGGTACATTAATGAGCACTCAGG 2460  
Qy 2461 AAAGATCTCGTTACTGGAAGTTAGCACTTAAGGAGGCAAAAGCAGAACCAATTAAT 2520  
Db 2461 AAAGATCTCGTTACTGGAAGTTAGCACTTAAGGAGGCAAAAGCAGAACCAATTAAT 2520  
Qy 2521 GTGTGAGTCAAGTGTGCAAGCATTTGAAAACCCCAAGGACTAATTAATGTTGTTCCAAAG 2580  
Db 2521 GTGTGAGTCAAGTGTGCAAGCATTTGAAAACCCCAAGGACTAATTAATGTTGTTCCAAAG 2580  
Qy 2581 ATTAATGAAGTGAACAGAGGCTTTAAGTATCACTTGGGACATGAAGTTAACACAGATC 2640  
Db 2581 ATTAATGAAGTGAACAGAGGCTTTAAGTATCACTTGGGACATGAAGTTAACACAGATC 2640

Db 2640 ATTAATGAAGTGAACAGAGGCTTTAAGTATCACTTGGGACATGAAGTTAACACAGATC 2640  
Qy 2641 GGGAAACAGAGATGAAGATGGAAGAGTGAATTTGATGCTCAGATTTTGGAGATACAT 2700  
Db 2641 GGGAAACAGAGATGAAGATGGAAGAGTGAATTTGATGCTCAGATTTTGGAGATACAT 2700  
Qy 2701 TCAAGTTTCAAAACGCGCAGTCAATTTGCTCTGTTTTCAATTCAGAAATCAGAAAGAGG 2760  
Db 2701 TCAAGTTTCAAAACGCGCAGTCAATTTGCTCTGTTTTCAATTCAGAAATCAGAAAGAGG 2760  
Qy 2761 AATGTGCAACATCTCTGCCCCACCTGAGGCTCTTAAGAAACCAAGTCCAAAGTCACTT 2820  
Db 2761 AATGTGCAACATCTCTGCCCCACCTGAGGCTCTTAAGAAACCAAGTCCAAAGTCACTT 2820  
Qy 2821 TTGAATGTGAACAAAGAGAGAAATCAAGGAAAGAAATGAATTAATCAAGCTGTAC 2880  
Db 2821 TTGAATGTGAACAAAGAGAGAAATCAAGGAAAGAAATGAATTAATCAAGCTGTAC 2880  
Qy 2881 AGACAGTAAATATCATCTGAGGCTTCTGAGTGTGTCAGAAAGATTAAGCCAGTTGATA 2940  
Db 2881 AGACAGTAAATATCATCTGAGGCTTCTGAGTGTGTCAGAAAGATTAAGCCAGTTGATA 2940  
Qy 2941 ATGCCAAATGTATATCAAGAGAGGCTTAAGTGTGTTATCATCTCAAGTTCAAGAGCA 3000  
Db 2941 ATGCCAAATGTATATCAAGAGAGGCTTAAGTGTGTTATCATCTCAAGTTCAAGAGCA 3000  
Qy 3001 ACGAACTGAGCTCTATTAATCAATTAATCAATGACATTTTCAAAACCAATATCTATAC 3060  
Db 3001 ACGAACTGAGCTCTATTAATCAATTAATCAATGACATTTTCAAAACCAATATCTATAC 3060  
Qy 3061 CACCACTTTTCCCATCAAGTCAATTTGTTAAACAAATGTAAGAAATCTGCTAGAGG 3120  
Db 3061 CACCACTTTTCCCATCAAGTCAATTTGTTAAACAAATGTAAGAAATCTGCTAGAGG 3120  
Qy 3121 AAAACTTTGAGAAACATTCATGATGTCACCTGAAGAGAAATGGAATGAGAAATTCGAA 3180  
Db 3121 AAAACTTTGAGAAACATTCATGATGTCACCTGAAGAGAAATGGAATGAGAAATTCGAA 3180  
Qy 3181 GTACAGTGAAGCAATTAAGCCGTATTAATTAAGAAATGTTTTTAAAGAGCCAGCT 3240  
Db 3181 GTACAGTGAAGCAATTAAGCCGTATTAATTAAGAAATGTTTTTAAAGAGCCAGCT 3240  
Qy 3241 CAAGCAATTAATTAAGAGTGAAGTCCAGTACTTAATGAAGTGGGCTCCAGATTAATGAAA 3300  
Db 3241 CAAGCAATTAATTAAGAGTGAAGTCCAGTACTTAATGAAGTGGGCTCCAGATTAATGAAA 3300  
Qy 3301 TAGGTTCCAGTGAAGAAACATTCAGAGAGAACTAGTGAAGAAACAGAGGCCAAATTTGA 3360  
Db 3301 TAGGTTCCAGTGAAGAAACATTCAGAGAGAACTAGTGAAGAAACAGAGGCCAAATTTGA 3360  
Qy 3361 ATGCTATGCTTAAGATTAGGGGTTTTGCAACTGAGGCTTATTAACAAAGTCTTCTGAAA 3420  
Db 3361 ATGCTATGCTTAAGATTAGGGGTTTTGCAACTGAGGCTTATTAACAAAGTCTTCTGAAA 3420  
Qy 3421 GTAATTTGAACATCTGAAATTAAGAAAGCAAGAAATGAAGAAAGTACTGAGATGTTA 3480  
Db 3421 GTAATTTGAACATCTGAAATTAAGAAAGCAAGAAATGAAGAAAGTACTGAGATGTTA 3480  
Qy 3481 ATACAGATTTCTCTCATATCTGATTTAGATTAATCTTAAGAAACAGGCTATGGAATATGTC 3540  
Db 3481 ATACAGATTTCTCTCATATCTGATTTAGATTAATCTTAAGAAACAGGCTATGGAATATGTC 3540  
Qy 3541 ATGCATCTCAGGTTGTTCTGAGACACTGTATGACCTGTATGATGATGTTGAAATTAAGG 3600  
Db 3541 ATGCATCTCAGGTTGTTCTGAGACACTGTATGACCTGTATGATGATGTTGAAATTAAGG 3600  
Qy 3601 AAAGATCTAGTTTGTCTGAAATGAACATTAAGAAAGTTCGCTTTTAAAGCAAAAGCG 3660  
Db 3601 AAAGATCTAGTTTGTCTGAAATGAACATTAAGAAAGTTCGCTTTTAAAGCAAAAGCG 3660  
Qy 3661 TCCAGAGAGAGAGGTTAGCAGAGAGTCTTACCCCTTCAACCATATCAATTTGGCTCAGG 3720  
Db 3661 TCCAGAGAGAGAGGTTAGCAGAGAGTCTTACCCCTTCAACCATATCAATTTGGCTCAGG 3720

OY	3721	GTAAACGAAGAGGGGCGCAAGAAATTAGATGCTCTCAGAAAGAACTTAATCTAGTAGAGATG	3780
Db	3721	GTAAACGAAGAGGGGCGCAAGAAATTAGATGCTCTCAGAAAGAACTTAATCTAGTAGAGATG	3780
OY	3781	AAGAGCTTCCCTGCTCCACAACCTTGTAATTGGAATGTAAACATPTACCTTCAGT	3840
Db	3781	AAGAGCTTCCCTGCTCCACAACCTTGTAATTGGAATGTAAACATPTACCTTCAGT	3840
OY	3841	CTACTAGGCATATAGCAACCGTTGCTACCGAGTGTCTGTCTAAAGAACACAGAGAGAAATTAT	3900
Db	3841	CTACTAGGCATATAGCAACCGTTGCTACCGAGTGTCTGTCTAAAGAACACAGAGAGAAATTAT	3900
OY	3901	TATCATTTGAAGAAATGCTTAAATATGATCTGACGTAAACAGTAAATATGCAAAAGGCATCTC	3960
Db	3901	TATCATTTGAAGAAATGCTTAAATATGATCTGACGTAAACAGTAAATATGCAAAAGGCATCTC	3960
OY	3961	AGGAACATCACCCTTAATAGTAGAGAAACAAATGTTCTGCTAAGCTTGTTCCTCAAGTGCA	4020
Db	3961	AGGAACATCACCCTTAATAGTAGAGAAACAAATGTTCTGCTAAGCTTGTTCCTCAAGTGCA	4020
OY	4021	GTGAATTGGAAGACTTGAACGAAATACAAACACCCAGAGATCCTTCTCTGATGGTCTT	4080
Db	4021	GTGAATTGGAAGACTTGAACGAAATACAAACACCCAGAGATCCTTCTCTGATGGTCTT	4080
OY	4081	CCAAACAAATGAGGATCAGTCTGAAAGCCAGGAGTGGTCTGATGACAGGAATTTG	4140
Db	4081	CCAAACAAATGAGGATCAGTCTGAAAGCCAGGAGTGGTCTGATGACAGGAATTTG	4140
OY	4141	TTTCAGATGATGAAAGAAAGAGAAAGGGCTTGGAAAGAAATATATCAGAAAGCAAGCA	4200
Db	4141	TTTCAGATGATGAAAGAAAGAGAAAGGGCTTGGAAAGAAATATCAGAAAGCAAGCA	4200
OY	4201	TGGATTCCAACTTAGTGAGAGAGCATCTGGGTGTGAGAGTGAACAAGCGCTCTGAG	4260
Db	4201	TGGATTCCAACTTAGTGAGAGAGCATCTGGGTGTGAGAGTGAACAAGCGCTCTGAG	4260
OY	4261	ACTGCTCAGGGCTATCTCTCTAGATGACATTTTAAACCACTCAGCAGAGGATACCATGC	4320
Db	4261	ACTGCTCAGGGCTATCTCTCTAGATGACATTTTAAACCACTCAGCAGAGGATACCATGC	4320
OY	4321	AACATTAACCTGATTAAGTCCAGCAGGAATGCTGAACCTAGAACTGTGTGTAACAACG	4380
Db	4321	AACATTAACCTGATTAAGTCCAGCAGGAATGCTGAACCTAGAACTGTGTGTAACAACG	4380
OY	4381	ATGGGAGCAGCGCTTCTAACAAGCTAACCCCTTCATCACTAAGTACCTCTCGCCCTTAGG	4440
Db	4381	ATGGGAGCAGCGCTTCTAACAAGCTAACCCCTTCATCACTAAGTACCTCTCGCCCTTAGG	4440
OY	4441	ACCTGCGAAATCCAGAACAAAGCAATCAGAAAAAAGCAGTATTAACTTACAGAAAAAGTA	4500
Db	4441	ACCTGCGAAATCCAGAACAAAGCAATCAGAAAAAAGCAGTATTAACTTACAGAAAAAGTA	4500
OY	4501	GTGAATACCTTAATAAGCCAGAAATCCAGAAAGCGCTTCTGCTGACAAAGTTGAGGTCTG	4560
Db	4501	GTGAATACCTTAATAAGCCAGAAATCCAGAAAGCGCTTCTGCTGACAAAGTTGAGGTCTG	4560
OY	4561	CAGATAGTCTTACACAGTAAAAATTAAGAACACAGAGTGGAAAGGTCAATCCCTCTTAAT	4620
Db	4561	CAGATAGTCTTACACAGTAAAAATTAAGAACACAGAGTGGAAAGGTCAATCCCTCTTAAT	4620
OY	4621	GCCCATCATTAATGATGATAGTGTGTACATGACAGTGTCTGGAGAGTCTTACAGAAATGAA	4680
Db	4621	GCCCATCATTAATGATGATAGTGTGTACATGACAGTGTCTGGAGAGTCTTACAGAAATGAA	4680
OY	4681	ACTAACCCATCTCAAGAGAGGCTCATTTAAGTTGTAATGTGAGAGAGCAACAGCTGAGAG	4740
Db	4681	ACTAACCCATCTCAAGAGAGGCTCATTTAAGTTGTAATGTGAGAGAGCAACAGCTGAGAG	4740
OY	4741	AGTCTGGGCGCACGATTTTGAACGAAACTTCTTACTTCCCAAGCAAGATCTTACAGGAA	4800
Db	4741	AGTCTGGGCGCACGATTTTGAACGAAACTTCTTACTTCCCAAGCAAGATCTTACAGGAA	4800

QY	4801	CCCCCTACCTGGAAATCTGGAAATCAAGCCTCTTCTCTGTATGACCTCGAATCTGAATCTTCTCTG	4860
Db	4801	CCCCCTACCTGGAAATCTGGAAATCAAGCCTCTTCTCTGTATGACCTCGAATCTGAATCTTCTCTG	4860
QY	4861	AAGACAGAGCCCCAGAGTCAAGCTCGTGTGGCAATACATCATCTTCAACCTCTGCATTTGA	4920
Db	4861	AAGACAGAGCCCCAGAGTCAAGCTCGTGTGGCAATACATCATCTTCAACCTCTGCATTTGA	4920
QY	4921	AAGTTCCCAATTGAAAGTTGCAGAAATCTGCCCAGGGTCCAGCTGCTCATATCTA	4980
Db	4921	AAGTTCCCAATTGAAAGTTGCAGAAATCTGCCCAGGGTCCAGCTGCTCATATCTA	4980
QY	4991	ATACTGCTGGGTATATATGCAATGGAATAAAAGTGTGACAGAGGAGAAACCCAGAAATTTGACAG	5040
Db	4991	ATACTGCTGGGTATATATGCAATGGAATAAAAGTGTGACAGAGGAGAAACCCAGAAATTTGACAG	5040
QY	5041	CTTCACAACGAAAGGGTCAACAAAGAATATGCATATGATGTGTCTGCGGCTCAACCCCAAG	5100
Db	5041	CTTCACAACGAAAGGGTCAACAAAGAATATGCATATGATGTGTCTGCGGCTCAACCCCAAG	5100
QY	5101	AATTTATGCTGTGTACAAAGTTTCCAGAAAACACACATCATCTTTAACTAATCTAATTA	5160
Db	5101	AATTTATGCTGTGTACAAAGTTTCCAGAAAACACACATCATCTTTAACTAATCTAATTA	5160
QY	5161	CTGAAGAGACTACCTCAATGTTGTATATGAAAACAGATGCTGAGTTGTGTGTGTAACGGACAC	5220
Db	5161	CTGAAGAGACTACCTCAATGTTGTATATGAAAACAGATGCTGAGTTGTGTGTGTAACGGACAC	5220
QY	5221	TGAATATATTTCTAGAAATTCGGGAGAGAAAATGGTAGTAGTATTTCTGGGTGACCC	5280
Db	5221	TGAATATATTTCTAGAAATTCGGGAGAGAAAATGGTAGTAGTATTTCTGGGTGACCC	5280
QY	5281	AGTCTATTTAAAGAAAAGAAAATGCTGTGATGACATGATTTTGAAGTCAGAGAGAGATGTGG	5340
Db	5281	AGTCTATTTAAAGAAAAGAAAATGCTGTGATGACATGATTTTGAAGTCAGAGAGAGATGTGG	5340
QY	5341	TCATATGAGAAACACCAACCAAGTCCAAAGCAGAACAGAAATCCCAAGAACAGAAAGTCT	5400
Db	5341	TCATATGAGAAACACCAACCAAGTCCAAAGCAGAACAGAAATCCCAAGAACAGAAAGTCT	5400
QY	5401	TCAGAGGGGCTAGAAATCTGTTGCTATGAGGCGCTTCAACCAATGCCCCAGATCAACTGG	5460
Db	5401	TCAGAGGGGCTAGAAATCTGTTGCTATGAGGCGCTTCAACCAATGCCCCAGATCAACTGG	5460
QY	5461	AATGATATGTAACAGCTGTGTGTCTTCTGTGTGAAGAGCTTTCATCATTCACCTTG	5520
Db	5461	AATGATATGTAACAGCTGTGTGTCTTCTGTGTGAAGAGCTTTCATCATTCACCTTG	5520
QY	5521	GCAACAGGTCTCACCACTTGTGTTGTGTGACACCAATGCTCTGACAGAGACATATGGCT	5580
Db	5521	GCAACAGGTCTCACCACTTGTGTTGTGTGACACCAATGCTCTGACAGAGACATATGGCT	5580
QY	5581	TCATATGCAATTTGGGCAGATGTGTAGGCACTGTGTGTGACCCGAGATGGGTGTGGACA	5640
Db	5581	TCATATGCAATTTGGGCAGATGTGTAGGCACTGTGTGTGACCCGAGATGGGTGTGGACA	5640
QY	5641	GTGTAGCACTTACACAGTCCAGAGAGCTGACACTTACCTGATATCCCAAGATCCCCACA	5700
Db	5641	GTGTAGCACTTACACAGTCCAGAGAGCTGACACTTACCTGATATCCCAAGATCCCCACA	5700
QY	5701	GCCTACTACTGA 5711	
Db	5701	GCCTACTACTGA 5711	

RESULT 4  
US-09-962-828-3  
; Sequence 3, Application US/09962828  
; Publication NO. US20030022184A1  
; GENERAL INFORMATION:  
; APPLICANT: Murphy, Patricia D.  
; Allen, Annette C.  
; Alvaes, Christopher P.

Critz, Brenda S.  
Olson, Sheri J.  
Thurber, Denise  
Zeng, Bin  
TITLE OF INVENTION: Coding Sequences of the Human  
BRCA1 Gene  
NUMBER OF SEQUENCES: 72  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Morgan Lewis & Bockius LLP  
STREET: 1111 Pennsylvania Avenue N. W.  
CITY: Washington  
STATE: DC  
COUNTRY: USA  
ZIP: 20004  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/982,828  
FILING DATE: 22-Oct-2001  
CLASSIFICATION: <unknown>  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 09/074,453  
FILING DATE: 1998-05-06  
APPLICATION NUMBER: US 08/798,691  
FILING DATE: 1997-02-12  
APPLICATION NUMBER: US 08/598,591  
FILING DATE: 1996-02-12  
ATTORNEY/AGENT INFORMATION:  
NAME: Michael S. Tuscan  
REGISTRATION NUMBER: 43,210  
REFERENCE/DOCKET NUMBER: 44921-5053-01-US  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 202-739-3000  
TELEFAX: 202-739-3001  
INFORMATION FOR SEQ ID NO: 3:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 5711 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: not relevant  
TOPOLOGY: linear  
MOLECULE TYPE: cDNA  
ORIGINAL SOURCE:  
ORGANISM: Homo sapiens  
STRAIN: BRCA1 (om12)  
POSITION IN GENOME:  
CHROMOSOME/SEGMENT: 17  
MAP POSITION: 17q21  
SEQUENCE DESCRIPTION: SEQ ID NO: 3:  
US-09-982-828-3

Query Match 100.0%; Score 5709.4; DB 11; Length 5711;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 5710; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 AGCTGCTGAGACTTCTGGAACCCCGACCAAGGCTGTGGGGTTTCTCAGATACTGGGCC 60  
DB 1 AGCTGCTGAGACTTCTGGAACCCCGACCAAGGCTGTGGGGTTTCTCAGATACTGGGCC 60  
QY 61 CCTGGCTCAGAGAGCCTTCACTCTGTCTGTGGTAAAGTTCAATTGGAACGAAAGAAA 120  
DB 61 CCTGGCTCAGAGAGCCTTCACTCTGTCTGTGGTAAAGTTCAATTGGAACGAAAGAAA 120  
QY 121 TGGATTATCTGCTCTTGGCGTTGAAGAAGTACAATAATGTCATTAATGCTATGCGAGAAA 180  
DB 121 TGGATTATCTGCTCTTGGCGTTGAAGAAGTACAATAATGTCATTAATGCTATGCGAGAAA 180  
QY 181 TCTTAGAGTGTCCCATCTGTCTGAGATTGATCAAGAACTGTCTTCCAAGAGTGTGACC 240  
DB 181 TCTTAGAGTGTCCCATCTGTCTGAGATTGATCAAGAACTGTCTTCCAAGAGTGTGACC 240

QY 241 ACATATTTTGCATAATTTTGCATGCTGAAACTTCTCAACCAAGAGAAAGGGCTTCACAGT 300  
DB 241 ACATATTTTGCATAATTTTGCATGCTGAAACTTCTCAACCAAGAGAAAGGGCTTCACAGT 300  
QY 301 GTCTTTATGTGAATGATATTAACCAAGAGCCTTCAAGAAAGTACGAGATTAGTC 360  
DB 301 GTCTTTATGTGAATGATATTAACCAAGAGCCTTCAAGAAAGTACGAGATTAGTC 360  
QY 361 AACTTTGGAAGACCTATGAAATTCATTTGTGCTTTTCACTTGACACAGGTTTGAGT 420  
DB 361 AACTTTGGAAGACCTATGAAATTCATTTGTGCTTTTCACTTGACACAGGTTTGAGT 420  
QY 421 ATGCAAAACAGCTATATTTTGCATAAAGAAATTAATCTCTCTGAACATCTAAAGATG 480  
DB 421 ATGCAAAACAGCTATATTTTGCATAAAGAAATTAATCTCTCTGAACATCTAAAGATG 480  
QY 481 AAGTTTCTATCATCCAAAGTATGAGCTACAGAAACCGTGCCAAAGACTTCTACAGATG 540  
DB 481 AAGTTTCTATCATCCAAAGTATGAGCTACAGAAACCGTGCCAAAGACTTCTACAGATG 540  
QY 541 AACCAGAAATCCCTTCTCTGAGAGAAACCAAGTCTCAGTCCCACTCTTAACCTTGGAA 600  
DB 541 AACCAGAAATCCCTTCTCTGAGAGAAACCAAGTCTCAGTCCCACTCTTAACCTTGGAA 600  
QY 601 CTGTGAGAACTCTGAGAGCAAGCAGCGGATACCACTCAAAAGACGTCTGTCTACATTG 660  
DB 601 CTGTGAGAACTCTGAGAGCAAGCAGCGGATACCACTCAAAAGACGTCTGTCTACATTG 660  
QY 661 AATTGGATCTGATTCCTCTGAGAGTACCCGTTAATAGGCAACTTATTCAGTGTGGAG 720  
DB 661 AATTGGATCTGATTCCTCTGAGAGTACCCGTTAATAGGCAACTTATTCAGTGTGGAG 720  
QY 721 ATCAAGAAATTTGTACAAATCAACCCCTCAAGAGACAGGAGATGAATCAATTGTTCTG 780  
DB 721 ATCAAGAAATTTGTACAAATCAACCCCTCAAGAGACAGGAGATGAATCAATTGTTCTG 780  
QY 781 CAAAAAGGCTGCTGTGAAATTTTCTGAGAGGATGTAAACAAATCTGAACATCTCAAC 840  
DB 781 CAAAAAGGCTGCTGTGAAATTTTCTGAGAGGATGTAAACAAATCTGAACATCTCAAC 840  
QY 841 CCAGTAATATGATTTTGAACCACTGAGAGCGTGACGTGAGAGGATCCAGAAAAGT 900  
DB 841 CCAGTAATATGATTTTGAACCACTGAGAGCGTGACGTGAGAGGATCCAGAAAAGT 900  
QY 901 ATCAGGAGTATCTGTTTCAAACTTGCATGTGAGCCATGTGGCAAAATCTCAATGCA 960  
DB 901 ATCAGGAGTATCTGTTTCAAACTTGCATGTGAGCCATGTGGCAAAATCTCAATGCA 960  
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DB 1021 AGGCTGAATTTCTGATATTAAGCAAAACAGCTGTGCTTGAAGAGCCAACTAACAGAT 1080  
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DB 1081 GGGCTGGAAGTAAAGAAACATGTAATGATAGCGGACTCCAGCACAGAAAAAAGGTAG 1140  
QY 1141 ATCTGAATGCTATCCCTGTGTGAGAGAAAGAAATGAAATGAGCAAACTGCCATGCT 1200  
DB 1141 ATCTGAATGCTATCCCTGTGTGAGAGAAAGAAATGAAATGAGCAAACTGCCATGCT 1200  
QY 1201 CAGAGAATCTTGAAGATCTGAAGATGTTCTCTGGATTAACCTAAATAGCAGCATTCAGA 1260  
DB 1201 CAGAGAATCTTGAAGATCTGAAGATGTTCTCTGGATTAACCTAAATAGCAGCATTCAGA 1260  
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QY 1321 GGGAGTCTGAATCAAAATCCCAAGTACGATGATGATTTGAGCGTTCTAATAGATGATG 1380

1321 GGGAGTCTGAATCAATGCAATGCAAGAGCTGATGATTTGGAAGCTTCTAATATGAGTAGATG 1380  
1381 AATATTCGTGTTCTTCAGAGAAATATGACTTATCTGCGACAGATATCTCTAGAGGCTTTAA 1440  
1381 AATATTCGTGTTCTTCAGAGAAATATGACTTATCTGCGACAGATATCTCTAGAGGCTTTAA 1440  
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1441 TATGTAAGAGTGAAGAGTTCACCTCAATCAGTAGAGATATATTTGAAGCAAAATAT 1500  
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3421 GTAAATGTAAGACATTCAGAAATTAAGAAAGCAAGAAATTAAGAAAGTGAAGTGAAGTGAAGTGAAG 3480  
3481 ATACAGATTTCTCTCAATATCTGATTTCAAGTAACTTAAGAAAGAGCTATGGAAGTGAAGTGAAG 3540  
3481 ATACAGATTTCTCTCAATATCTGATTTCAAGTAACTTAAGAAAGAGCTATGGAAGTGAAGTGAAG 3540

OY	3541	ATGCATCTCAGGTTGTTCTGTAGACACCTGTATGACCTGTTAGATGATGCTAAATTAAG	3600
Db	3541	ATGCATCTCAGGTTGTTCTGTAGACACCTGTATGACCTGTTAGATGATGCTAAATTAAG	3600
OY	3601	AAGATACTAGTTTGTCTGAAATATGCACTTAAGGAAAGTTCTGCTGTTTATGCAAAAGCG	3660
Db	3601	AAGATACTAGTTTGTCTGAAATATGCACTTAAGGAAAGTTCTGCTGTTTATGCAAAAGCG	3660
OY	3661	TCGAGAGAGAGAGCTTGTAGCAGAGTCTTAGCCCTTTCACCCATACATTTGGCTCAGG	3720
Db	3661	TCGAGAGAGAGAGCTTGTAGCAGAGTCTTAGCCCTTTCACCCATACATTTGGCTCAGG	3720
OY	3721	GTTACCGAAGAGGGGCGCAAGAAATTAGTCTCTGAAAGAGACTTATCTAGTAGATG	3780
Db	3721	GTTACCGAAGAGGGGCGCAAGAAATTAGTCTCTGAAAGAGACTTATCTAGTAGATG	3780
OY	3781	AAGAGCTTCCGCGCTTCCAAACCTTGTAATTGTAATTAAGTAATATATACCTCTCAGT	3840
Db	3781	AAGAGCTTCCGCGCTTCCAAACCTTGTAATTGTAATTAAGTAATATATACCTCTCAGT	3840
OY	3841	CTACTAGGCATATAGCACCGCTTGCTACCGAGTGTCTGTCTTAAGAACACAGAGAAATTAAT	3900
Db	3841	CTACTAGGCATATAGCACCGCTTGCTACCGAGTGTCTGTCTTAAGAACACAGAGAAATTAAT	3900
OY	3901	TATCATTTGAAGATATGCTTAAATATGCTGACAGTAAACAGTAAATATGGCAAGGCATCTC	3960
Db	3901	TATCATTTGAAGATATGCTTAAATATGCTGACAGTAAACAGTAAATATGGCAAGGCATCTC	3960
OY	3961	AGGAATCATCCTTATGTAAGGAAACAAATATGTTCTGTAAGCTGTTTCTTTCACAGTGCA	4020
Db	3961	AGGAATCATCCTTATGTAAGGAAACAAATATGTTCTGTAAGCTGTTTCTTTCACAGTGCA	4020
OY	4021	GTTGAATTTGAAGACTTGACTGCAAAATACAAACCCAGAGTCCCTTCTGATTTGGTCTT	4080
Db	4021	GTTGAATTTGAAGACTTGACTGCAAAATACAAACCCAGAGTCCCTTCTGATTTGGTCTT	4080
OY	4081	CCAAACAAATGAGGCATCATGCTGTAAGCCAGGAGTTGGTCTGTAGTGCACAGGAATTTGG	4140
Db	4081	CCAAACAAATGAGGCATCATGCTGTAAGCCAGGAGTTGGTCTGTAGTGCACAGGAATTTGG	4140
OY	4141	TTTCAGATGATGAGAAAGAGGAACGGGCTTGGAAAGAAATTAATCAGAGAGCAAAACA	4200
Db	4141	TTTCAGATGATGAGAAAGAGGAACGGGCTTGGAAAGAAATTAATCAGAGAGCAAAACA	4200
OY	4201	TGGATTTCAACTTGGTGAAGCAGCATCTGGGTGTGAGAGTGAACAAAGCCTCTCTAAG	4260
Db	4201	TGGATTTCAACTTGGTGAAGCAGCATCTGGGTGTGAGAGTGAACAAAGCCTCTCTAAG	4260
OY	4261	ACTGCTCAGGGCTATCTCTCTAGAGTGCATTTTAACACATCAGCAGAGGATACCATGC	4320
Db	4261	ACTGCTCAGGGCTATCTCTCTAGAGTGCATTTTAACACATCAGCAGAGGATACCATGC	4320
OY	4321	AACATTAACCTGATTAAGGCTTCAGCAGAAATGGCTGAATCTAGAAAGCTGTGTAAGACGC	4380
Db	4321	AACATTAACCTGATTAAGGCTTCAGCAGAAATGGCTGAATCTAGAAAGCTGTGTAAGACGC	4380
OY	4381	ATGGAGGCACGCTTCTTAACAGCTACCTTCTCATATAGTACCTCCCTCTGAGG	4440
Db	4381	ATGGAGGCACGCTTCTTAACAGCTACCTTCTCATATAGTACCTCCCTCTGAGG	4440
OY	4441	ACCTGCGAAATTCAGAAACAAAGCAGCATCAGAAAAAGCAGTATTAATCTTCAAGAAAAATA	4500
Db	4441	ACCTGCGAAATTCAGAAACAAAGCAGCATCAGAAAAAGCAGTATTAATCTTCAAGAAAAATA	4500
OY	4501	GTTGAATACCTATTAAGCCAGAAATCCAGAAAGGCTTTTCTGCTGACAAGTTTGAAGGTCTG	4560
Db	4501	GTTGAATACCTATTAAGCCAGAAATCCAGAAAGGCTTTTCTGCTGACAAGTTTGAAGGTCTG	4560
OY	4561	CAGATATGTTCTTACAGTAAATTAAGAACCAAGAGTGGAAAGGTCAATCCCTCTCTAAT	4620
Db	4561	CAGATATGTTCTTACAGTAAATTAAGAACCAAGAGTGGAAAGGTCAATCCCTCTCTAAT	4620

QY	4621	CCCCATCATTTGATGATATGCTGTGATACATGCAACAGTTCTCTGGAGATCTTCAAGATAGAA	4680
Db	4621	GCCCATCATTTGATGATGATGTGTACATGCAACAGTTCTCTGGAGATCTTCAAGATAGAA	4680
QY	4681	ACTACCCATCTCAAGAGAGCTCATTTAAGTGTGTGATGTGAGAGACCAACAGCTGGAA	4740
Db	4681	ACTACCCATCTCAAGAGAGAGCTCATTTAAGTGTGTGATGTGAGAGACCAACAGCTGGAA	4740
QY	4741	AGTCTGGGCCACACGATTTGACGGAAACATCTTACCTTGCAAGGCAAGATCTAGAGGAA	4800
Db	4741	AGTCTGGGCCACACGATTTGACGGAAACATCTTACCTTGCAAGGCAAGATCTAGAGGAA	4800
QY	4801	CCCCCTTACCTGGAAATCTGGAAATCAAGCTCTTCTCTGTATGACCTCGAATCTGATCTTCTG	4860
Db	4801	CCCCCTTACCTGGAAATCTGGAAATCAAGCTCTTCTCTGTATGACCTCGAATCTGATCTTCTG	4860
QY	4861	AAGACAGAGCCCCAGAGCTGAGCTGTGTGTGGCAATACCATCTTCAACCTCTGATTTGA	4920
Db	4861	AAGACAGAGCCCCAGAGCTGAGCTGTGTGTGGCAATACCATCTTCAACCTCTGATTTGA	4920
QY	4921	AAGTTCCCAATTGAAAGTTGACAGAAATCTGCCAGGGTCCAGCTGCTCTCATCTACTG	4980
Db	4921	AAGTTCCCAATTGAAAGTTGACAGAAATCTGCCAGGGTCCAGCTGCTCTCATCTACTG	4980
QY	4981	ATACTGCTGGGTATTAATGCAATGGAAGAAAGTGTAGACAGAGGAGACCCGAATTGACAG	5040
Db	4981	ATACTGCTGGGTATTAATGCAATGGAAGAAAGTGTAGACAGAGGAGACCCGAATTGACAG	5040
QY	5041	CTTCAACGAAGGGTCAACAAAGAAATGTCCATGTGTGTCTGTGGCTGACCCCAAG	5100
Db	5041	CTTCAACGAAGGGTCAACAAAGAAATGTCCATGTGTGTCTGTGGCTGACCCCAAG	5100
QY	5101	AATTTATGCTGTGTACAGATTTGCCAGAAAAACACATCATCTTTAATCTTAATTA	5160
Db	5101	AATTTATGCTGTGTACAGATTTGCCAGAAAAACACATCATCTTTAATCTTAATTA	5160
QY	5161	CTGAAGACACTACTCATGTGTTTATGTAAACAGATGTGTGATTTGTGTGAACGAC	5220
Db	5161	CTGAAGACACTACTCATGTGTTTATGTAAACAGATGTGTGATTTGTGTGAACGAC	5220
QY	5221	TGAAATATTTTCTTGAGAAATGCCGGAGAAAAATGGATGATTTCTGGGTGACC	5280
Db	5221	TGAAATATTTTCTTGAGAAATGCCGGAGAAAAATGGATGATTTCTGGGTGACC	5280
QY	5281	AGTCTATTAAGAAAGAAAAATGCTGATGATGACATGATTTTGAAGTCAAGAGAGATGCTGG	5340
Db	5281	AGTCTATTAAGAAAGAAAAATGCTGATGATGACATGATTTTGAAGTCAAGAGAGATGCTGG	5340
QY	5341	TCAAATGGAAGAAACCAACCAAGGTCCAAAGCGAGCAGAGAGATCCCAAGACAGAAAGTCT	5400
Db	5341	TCAAATGGAAGAAACCAACCAAGGTCCAAAGCGAGCAGAGAGATCCCAAGACAGAAAGTCT	5400
QY	5401	TCAGGGGGCTTGAAATCTGTGTCATATGGGCCCTTACCAACATGCCCACAGATCACTGG	5460
Db	5401	TCAGGGGGCTTGAAATCTGTGTCATATGGGCCCTTACCAACATGCCCACAGATCACTGG	5460
QY	5461	AATGGAATGGAATCAAGCTGTGTGTGTCCTGTGTGTGAAGAGCTTCACTTACCTTGCCTTG	5520
Db	5461	AATGGAATGGAATCAAGCTGTGTGTGTCCTGTGTGTGAAGAGCTTCACTTACCTTGCCTTG	5520
QY	5521	GCAACAGGTGTCCACCAATGTGTGTTGTGACGCCAGATGCTGTGACAGAGACAAATGGCT	5580
Db	5521	GCAACAGGTGTCCACCAATGTGTGTTGTGACGCCAGATGCTGTGACAGAGACAAATGGCT	5580
QY	5581	TCATATGCAATTTGGGCAAGTGTGTGAGCACTGTGTGTGACCCCAAGATGGGTGTGTGACA	5640
Db	5581	TCATATGCAATTTGGGCAAGTGTGTGAGCACTGTGTGTGACCCCAAGATGGGTGTGTGACA	5640
QY	5641	GTTGATGACCTTACAGAGTCCAGAGAGCTGACATCTACCTGATATCCCAATCCCCCACA	5700
Db	5641	GTTGATGACCTTACAGAGTCCAGAGAGCTGACATCTACCTGATATCCCAATCCCCCACA	5700
QY	5701	GCCACTACTGA 5711	





QY 1201 CAGAGAACTCTAGAGATCTGAAAGATGTTCTTGGATTAACACTAAATAGCAGACTTCAGA 1260  
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DB 1261 AAGTTAATGAGTGGTTTTCCAGAAAGTGAATGTAAGTTAGTTCTGATGATCTCAGATGATG 1320  
QY 1321 GGGAGTCTGATCAAAAGCCCAAGTGAATGTAATGGAGCTTCTAAATGAAGTGAATG 1380  
DB 1321 GGGAGTCTGATCAAAAGCCCAAGTGAATGTAATGGAGCTTCTAAATGAAGTGAATG 1380  
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DB 1381 AATATCTGTTCTTCCAGAGAAAATAGACTTACTGAGCAGTATCTCATGAGGCTTTAA 1440  
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DB 1681 CAGATTTGGCAGTTCAAAAAGACTCCTGAATGATTAATCAGGAACTTAACCAACGAGC 1740  
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DB 1741 AGAATGCTCAAGTGAATTAATTAATAGTGCATGAGAAATTAACAAAGGTGAT 1800  
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DB 1801 CTATTCAGAAATGAGAAAAATCTTAACCCAAATGATCACTCGAAAAAAGATCTGTTTCA 1860  
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DB 1921 ACAATTTCAAAGCACTTAAGAAAGTAAGGCTGAGAGAACTTTCTACCGAGCATATTC 1980  
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DB 2641 GGAAGAACAGCATGAATGAAGAAAGTGAACCTTGATGCTCAGTATTTGCAAGATACAT 2700  
QY 2701 TCAAGGTTTCAAGCGCAGTCAATTTGCTGTTTTCAAATCCAGAAATGCAAGAGG 2760  
DB 2701 TCAAGGTTTCAAGCGCAGTCAATTTGCTGTTTTCAAATCCAGAAATGCAAGAGG 2760  
QY 2761 AATGTCAACATTTCTGCCCCACTCTGAGTCTTTAAAGAAACAAAGTCCAAAGTCACTT 2820  
DB 2761 AATGTCAACATTTCTGCCCCACTCTGAGTCTTTAAAGAAACAAAGTCCAAAGTCACTT 2820  
QY 2821 TTGAATGGAACAAAGAGAAAGAAATCAAGGAAGAAATGAGTCAATTAATCAAGCTGTAC 2880  
DB 2821 TTGAATGGAACAAAGAGAAAGAAATCAAGGAAGAAATGAGTCAATTAATCAAGCTGTAC 2880  
QY 2881 AGACAGTTAATATCATGTCAGAGCTTTCTGTGTTGGTCAAGAAAGATAGCCAGTTGATA 2940  
DB 2881 AGACAGTTAATATCATGTCAGAGCTTTCTGTGTTGGTCAAGAAAGATAGCCAGTTGATA 2940  
QY 2941 ATGCCAAATGTAATCAAGAGAGGCTCTAGTCTTGTCTATCTCATGTCAGAGGCA 3000  
DB 2941 ATGCCAAATGTAATCAAGAGAGGCTCTAGTCTTGTCTATCTCATGTCAGAGGCA 3000  
QY 3001 ACGAAACTGACCTCATTAATCTCAAAATTAACAATGACCTTTTACAAAACCATATGATATC 3060  
DB 3001 ACGAAACTGACCTCATTAATCTCAAAATTAACAATGACCTTTTACAAAACCATATGATATC 3060  
QY 3061 CACCACTTTTCCCATCAAGTCAATTTGTAAACCTAAATGTAAGAAATCTGCTAGAGG 3120  
DB 3061 CACCACTTTTCCCATCAAGTCAATTTGTAAACCTAAATGTAAGAAATCTGCTAGAGG 3120  
QY 3121 AAAAATTGAGGAACATTCAATGTCACCTGAAAGAAAGTGGAAATGAGAACATTTCAA 3180  
DB 3121 AAAAATTGAGGAACATTCAATGTCACCTGAAAGAAAGTGGAAATGAGAACATTTCAA 3180  
QY 3181 GTACAGTGAAGCAATTAAGCCGTATTAACCTTAGAGAAAGTTTTAAAGAGCCAGCT 3240  
DB 3181 GTACAGTGAAGCAATTAAGCCGTATTAACCTTAGAGAAAGTTTTAAAGAGCCAGCT 3240  
QY 3241 CAAGCAATTAATTAAGTGAAGTCTCAGTACTAATGAAGTGGCTCAGATTAATATGAA 3300  
DB 3241 CAAGCAATTAATTAAGTGAAGTCTCAGTACTAATGAAGTGGCTCAGATTAATATGAA 3300  
QY 3301 TAGGTTCCAGTATGAAGAAACATTCAGCAGAACTAGGTAGAAACAGAGGCGCAAAATTTGA 3360  
DB 3301 TAGGTTCCAGTATGAAGAAACATTCAGCAGAACTAGGTAGAAACAGAGGCGCAAAATTTGA 3360  
QY 3361 ATGCTATGCTTAAGTTAGGGGTTTTGCAACCTGAGGCTATTAACAAAGTCTTCTGGA 3420

Db	3361	ATGCTATGCTTAGATTAGGGGTTTTCGAACTTGAGGCTCTATTAACAAGTCTTCTCGTGA	3420
QY	3421	GTAAATGTAGAGCATCTGAAATATAAAAGCAAGATATGAGAGTAGTTCAGACTGTAA	3480
Db	3421	GTAAATGTAGAGCATCTGAAATATAAAAGCAAGATATGAGAGTAGTTCAGACTGTAA	3480
QY	3481	ATACAGATTTCTCTCCATATCTGATTTCAATTAAGTTCAGACAGCTTATGGGAATGATC	3540
Db	3481	ATACAGATTTCTCTCCATATCTGATTTCAATTAAGTTCAGACAGCTTATGGGAATGATC	3540
QY	3541	ATGCATCTAGGTTTGTTGTGAGACCCGATGACCTGTATATGATGTGAATAAAGG	3600
Db	3541	ATGCATCTAGGTTTGTTGTGAGACCCGATGACCTGTATATGATGTGAATAAAGG	3600
QY	3601	AAGATACTAGTTTGTGCTGAAAATGACATTAAGAAAAGTCTGCTTTTATAGCAAAACG	3660
Db	3601	AAGATACTAGTTTGTGCTGAAAATGACATTAAGAAAAGTCTGCTTTTATAGCAAAACG	3660
QY	3661	TCCAGAGAGAGAGCTTAGCAGAGTCTTACGCTTTTCAACCCATACACATTTGGCTCAGG	3720
Db	3661	TCCAGAGAGAGAGCTTAGCAGAGTCTTACGCTTTTCAACCCATACACATTTGGCTCAGG	3720
QY	3721	GTACCCGAAAGAGGGGCGAAGAAATTAAGAGTCCCTCAGAAAGAACTTATCTAGTAGATG	3780
Db	3721	GTACCCGAAAGAGGGGCGAAGAAATTAAGAGTCCCTCAGAAAGAACTTATCTAGTAGATG	3780
QY	3781	AAGAGCTTCCCTGCTTCCAACTGTATTTGTAAAGTAAACAATATACCTTCTCAGT	3840
Db	3781	AAGAGCTTCCCTGCTTCCAACTGTATTTGTAAAGTAAACAATATACCTTCTCAGT	3840
QY	3841	CTACTAGGCAATGCAACCGTTGCTTACCGAGTGTCTGTCTTAAGAACACAGAGAGAAATTTAT	3900
Db	3841	CTACTAGGCAATGCAACCGTTGCTTACCGAGTGTCTGTCTTAAGAACACAGAGAGAAATTTAT	3900
QY	3901	TATCATTTGAAGAAATAGCTTAAATAGTCTGAGTAACCAAGTAAATATGGCAAAAGGATCTC	3960
Db	3901	TATCATTTGAAGAAATAGCTTAAATAGTCTGAGTAACCAAGTAAATATGGCAAAAGGATCTC	3960
QY	3961	AGGAACATCACCTTAGTAGAGGAAACAAAATGTTCTGAGTCTGTTTCTTCAACAGTSCA	4020
Db	3961	AGGAACATCACCTTAGTAGAGGAAACAAAATGTTCTGAGTCTGTTTCTTCAACAGTSCA	4020
QY	4021	GTGAATTTGGAGACCTTGAACCTGCAATATACAAACACCAGAGATCCTTCTTGAATGGTCTT	4080
Db	4021	GTGAATTTGGAGACCTTGAACCTGCAATATACAAACACCAGAGATCCTTCTTGAATGGTCTT	4080
QY	4081	CCAAACAATGAGGATCATGTCGTGAAGCCAGGAGTTGGTCTGAGTCAACAAGATTGG	4140
Db	4081	CCAAACAATGAGGATCATGTCGTGAAGCCAGGAGTTGGTCTGAGTCAACAAGATTGG	4140
QY	4141	TTTCAGATGATGAAGAAAGAGAAAGGGCTTGAAGAAATATATMAAGAGCAAGCA	4200
Db	4141	TTTCAGATGATGAAGAAAGAGAAAGGGCTTGAAGAAATATATMAAGAGCAAGCA	4200
QY	4201	TGGAATTCAAACTTAGTGAAGACAGCATCTGGGTGTGAGAGTGAACAAGCCTTCTGAG	4260
Db	4201	TGGAATTCAAACTTAGTGAAGACAGCATCTGGGTGTGAGAGTGAACAAGCCTTCTGAG	4260
QY	4261	ACTGCTCAGGGGTATCTCTCTCAGAGTGAATTTTAAACATCTCAGAGAGGATATACATGC	4320
Db	4261	ACTGCTCAGGGGTATCTCTCTCAGAGTGAATTTTAAACATCTCAGAGAGGATATACATGC	4320
QY	4321	AACATTAACCTGATTAAGCTCCAGCAGAAATGGCTGAACCTGAAGCTGTGTTAGAACGC	4380
Db	4321	AACATTAACCTGATTAAGCTCCAGCAGAAATGGCTGAACCTGAAGCTGTGTTAGAACGC	4380
QY	4381	ATGGAGGCAAGCTTCTTAACAGCTACCTTCATCATTAAGTACTCTCTGCTCCTTAGG	4440
Db	4381	ATGGAGGCAAGCTTCTTAACAGCTACCTTCATCATTAAGTACTCTCTGCTCCTTAGG	4440
QY	4441	ACCTGCGAAATTCAGAACCAAGACATCAGAAAAGCGATTAATCTTACAGAAAAGTA	4500
Db	4441	ACCTGCGAAATTCAGAACCAAGACATCAGAAAAGCGATTAATCTTACAGAAAAGTA	4500

Db	4441	ACCTGGAAATTCAGAACAAAGC	ATCAGAAAAACGATTAATCTTACAGAAAAAGTA	4500
QY	4501	GTGAATACCCTATTAAGCCAGAA	TCCAGAAAGCCCTTCTGTGACAAAGTTGAGGTCGTG	4560
Db	4501	GTGAATACCCTATTAAGCCAGAA	TCCAGAAAGCCCTTCTGTGACAAAGTTGAGGTCGTG	4560
QY	4561	CAGATAGTTCTACCACTA	AAAAATAAAGAACCAAGAGTGAAGGTCATCCCTCTTAAT	4620
Db	4561	CAGATAGTTCTACCACTA	AAAAATAAAGAACCAAGAGTGAAGGTCATCCCTCTTAAT	4620
QY	4621	GGCCATCAATTGATGATATAGTG	GTGTCAAGCAAGTGTCTGTGGAGTCTTGAGATAGAA	4680
Db	4621	GGCCATCAATTGATGATATAGTG	GTGTCAAGCAAGTGTCTGTGGAGTCTTGAGATAGAA	4680
QY	4681	ACTACCCACTTCAAGAGAGC	TCATTAAGTTGTGATGTGAGAGCAACAGCTGGAAG	4740
Db	4681	ACTACCCACTTCAAGAGAGC	TCATTAAGTTGTGATGTGAGAGCAACAGCTGGAAG	4740
QY	4741	AGTCTGGGCCACACGATTTGA	CCGAAACATCTTACTTCCAAAGCCAAAGATCTAAGGGAA	4800
Db	4741	AGTCTGGGCCACACGATTTGA	CCGAAACATCTTACTTCCAAAGCCAAAGATCTAAGGGAA	4800
QY	4801	CCCCCTTACCTGGAATCTTGGA	ATCTGGAATTCAGCCCTCTCTCTGTAGAACCTCGAATCTGTATCTCTG	4860
Db	4801	CCCCCTTACCTGGAATCTTGGA	ATCTGGAATTCAGCCCTCTCTCTGTAGAACCTCGAATCTGTATCTCTG	4860
QY	4861	AAGACAGAGCCCAAGAGTCA	GTCTGTGTGGCAACATCCATCTTCAACCTCTGCATTTGA	4920
Db	4861	AAGACAGAGCCCAAGAGTCA	GTCTGTGTGGCAACATCCATCTTCAACCTCTGCATTTGA	4920
QY	4921	AAGTTCCCAATTGAAAGTTG	CAAGATCTGCCAAGGTCACGCTGTGTCTATCTACTG	4980
Db	4921	AAGTTCCCAATTGAAAGTTG	CAAGATCTGCCAAGGTCACGCTGTGTCTATCTACTG	4980
QY	4981	ATATCTGCTGGGTATTAATG	CAATGGAAGAAATGTGAGAGGAGAAACCCAGAAATTGACAG	5040
Db	4981	ATATCTGCTGGGTATTAATG	CAATGGAAGAAATGTGAGAGGAGAAACCCAGAAATTGACAG	5040
QY	5041	CTTCAACAGAAAGGTCACAA	AAAAAGAAATGTCCATGTGTGTCTGTGGCCCTGACCCACAGAG	5100
Db	5041	CTTCAACAGAAAGGTCACAA	AAAAAGAAATGTCCATGTGTGTCTGTGGCCCTGACCCACAGAG	5100
QY	5101	AATTTATGCTGTGTGACA	AGTTTGCCAGAAAAACAACAATCACTTAACTTAATTA	5160
Db	5101	AATTTATGCTGTGTGACA	AGTTTGCCAGAAAAACAACAATCACTTAACTTAATTA	5160
QY	5161	CTGAAGAGACTACTCATGT	GTGTATGAAACACAGATGCTGAGTTGTGTGTGAACGCAAC	5220
Db	5161	CTGAAGAGACTACTCATGT	GTGTATGAAACACAGATGCTGAGTTGTGTGTGAACGCAAC	5220
QY	5221	TGAATAATATTTCTAGAA	TTGCGGAGAGAAATGGTATAGTATTTCTGGGCTGACCC	5280
Db	5221	TGAATAATATTTCTAGAA	TTGCGGAGAGAAATGGTATAGTATTTCTGGGCTGACCC	5280
QY	5281	AGTCTATTTAAAGAA	AAAAATGCTGATGATGACATGATTTTGAAGTCAGAGAGATGTGG	5340
Db	5281	AGTCTATTTAAAGAA	AAAAATGCTGATGATGACATGATTTTGAAGTCAGAGAGATGTGG	5340
QY	5341	TCAATGGAAGAAACCA	CCAGAGTCCAAAGCGACAGACAAAGATCCACGAGACAAAGATCT	5400
Db	5341	TCAATGGAAGAAACCA	CCAGAGTCCAAAGCGACAGACAAAGATCCACGAGACAAAGATCT	5400
QY	5401	TCAGGGGGCTAGAAATCT	GTGTGCTATGAGGCCCTTCAACCAACATGCCCACAGATTAACCTGG	5460
Db	5401	TCAGGGGGCTAGAAATCT	GTGTGCTATGAGGCCCTTCAACCAACATGCCCACAGATTAACCTGG	5460
QY	5461	AATGGAATGTAACA	CTGTGTGTGCTTCTGTGTGGAAGAGCTTTCATCAATTCACCTTG	5520
Db	5461	AATGGAATGTAACA	CTGTGTGTGCTTCTGTGTGGAAGAGCTTTCATCAATTCACCTTG	5520
QY	5521	GCAACAGGTGTCACCA	ATTGTGTTGTGACCCAGATGCTTGACAGAGACAAATGAGCT	5580
Db	5521	GCAACAGGTGTCACCA	ATTGTGTTGTGACCCAGATGCTTGACAGAGACAAATGAGCT	5580



Db 1021 AGGCTGAATTCGTATATAAAGCAACAGCTGGCTTAGCAAGAGCCAACTAACAGAT 1080  
Qy 1081 GGGCTGGAAGTAAAGAAATGAATGAGCGGCTCCGACGACAGAAAAAAGTNG 1140  
Db 1081 GGGCTGGAAGTAAAGAAATGAATGAGCGGCTCCGACGACAGAAAAAAGTNG 1140  
Qy 1141 ATCTGAATGCTGATCCCTGTGTGAGAGAAAAAGATGAATAGCAGAACTGCCATGCT 1200  
Db 1141 ATCTGAATGCTGATCCCTGTGTGAGAGAAAAAGATGAATAGCAGAACTGCCATGCT 1200  
Qy 1201 CAGAGAACTCTGAGACTCTGAAGATGTTCTTGATTAACCTAAATAGCAGATTCAGA 1260  
Db 1201 CAGAGAACTCTGAGACTCTGAAGATGTTCTTGATTAACCTAAATAGCAGATTCAGA 1260  
Qy 1261 AAGTTAATGAGTGGTTTTCCAGAGGATGAACCTGTTAGTCTGATGCTACATGATNG 1320  
Db 1261 AAGTTAATGAGTGGTTTTCCAGAGGATGAACCTGTTAGTCTGATGCTACATGATNG 1320  
Qy 1321 GGGAGCTGAATCAATGCGCAAGTAGCTGATGTAATGGAAGCTTCAATGAGTAGATG 1380  
Db 1321 GGGAGCTGAATCAATGCGCAAGTAGCTGATGTAATGGAAGCTTCAATGAGTAGATG 1380  
Qy 1381 AATATTCGTGTTCTTCAAGAAAAATGACTTACCTGAGGCTTCAATGAGGCTTTAA 1440  
Db 1381 AATATTCGTGTTCTTCAAGAAAAATGACTTACCTGAGGCTTCAATGAGGCTTTAA 1440  
Qy 1441 TATGTAAAGTAAAGAGTTCACTCCAAATCAGTAGAGTAAATTTGAAGCAAAATAT 1500  
Db 1441 TATGTAAAGTAAAGAGTTCACTCCAAATCAGTAGAGTAAATTTGAAGCAAAATAT 1500  
Qy 1501 TTGGGAAAACTATCGAAGAAAGGAGGAGCTCCCACTTAAGCATGTAATGCAAAATC 1560  
Db 1501 TTGGGAAAACTATCGAAGAAAGGAGGAGCTCCCACTTAAGCATGTAATGCAAAATC 1560  
Qy 1561 TAAATTAAGAGCACTTTGTTACTGAGCCACAGATTAATCAAGAGGCTCCCTCAAAATA 1620  
Db 1561 TAAATTAAGAGCACTTTGTTACTGAGCCACAGATTAATCAAGAGGCTCCCTCAAAATA 1620  
Qy 1621 AATTAAGGCTAAAGAGAGCACTACATCAGGCTTCACTGAGGATTTTATCAAGAAAG 1680  
Db 1621 AATTAAGGCTAAAGAGAGCACTACATCAGGCTTCACTGAGGATTTTATCAAGAAAG 1680  
Qy 1681 CAGATTTGGCAGTTCAAAAGACTCCTGAATGATTAATCAAGGAACTAACCCAAAGCAG 1740  
Db 1681 CAGATTTGGCAGTTCAAAAGACTCCTGAATGATTAATCAAGGAACTAACCCAAAGCAG 1740  
Qy 1741 AGAATGGTCAAGTGAATATTTACTAATAGTGTCAATGAGAAATTAACCAAAAGGTGAT 1800  
Db 1741 AGAATGGTCAAGTGAATATTTACTAATAGTGTCAATGAGAAATTAACCAAAAGGTGAT 1800  
Qy 1801 CTAATCAGAAATGAGAAAAATCTTAACCCAAATGATATCACTGAAAAAGATCTGCTTCA 1860  
Db 1801 CTAATCAGAAATGAGAAAAATCTTAACCCAAATGATATCACTGAAAAAGATCTGCTTCA 1860  
Qy 1861 AAAAGAAAGCTGAACCTTAAGCAGCAGTAAATGAGAAATGAGAACTGCAATTAATATCC 1920  
Db 1861 AAAAGAAAGCTGAACCTTAAGCAGCAGTAAATGAGAAATGAGAACTGCAATTAATATCC 1920  
Qy 1921 ACAATTTCAAAAGCAGCTTAAGAAATAGGCTGAGAGAAAGTCTTCAACAGGCAATATTC 1980  
Db 1921 ACAATTTCAAAAGCAGCTTAAGAAATAGGCTGAGAGAAAGTCTTCAACAGGCAATATTC 1980  
Qy 1981 ATGCGCTTGAATAGTACAGTGAAGATTAAGGAGGCACTTAATTTGATCTGAGAA 2040  
Db 1981 ATGCGCTTGAATAGTACAGTGAAGATTAAGGAGGCACTTAATTTGATCTGAGAA 2040  
Qy 2041 TTGATAGTTGTTCTAGCAGTGAAGATTAAGGAGGCACTTAATTTGATCTGAGAA 2100  
Db 2041 TTGATAGTTGTTCTAGCAGTGAAGATTAAGGAGGCACTTAATTTGATCTGAGAA 2100  
Qy 2101 GGCACAGCAAAACCTAACAATCATGAGAAAGTAAAGAACTGCAACTGAGAGCAAGAA 2160  
Db 2101 GGCACAGCAAAACCTAACAATCATGAGAAAGTAAAGAACTGCAACTGAGAGCAAGAA 2160

Qy 2161 GTAAACCCAAATGATGACAGCAAGTAAAGCATGACATGATTTCTCCAGAGCTGA 2220  
Db 2161 GTAAACCCAAATGATGACAGCAAGTAAAGCATGACATGATTTCTCCAGAGCTGA 2220  
Qy 2221 AGTTAACAATGACCTGGTCTTTTACTAGTGTCAATACAGTAGAATCTTAAGAAAT 2280  
Db 2221 AGTTAACAATGACCTGGTCTTTTACTAGTGTCAATACAGTAGAATCTTAAGAAAT 2280  
Qy 2281 TTGTCAATCTGAGCTTCCAGAGAGAGAAAAAGAGAAATGAGAAACAGTTAAAGTGT 2340  
Db 2281 TTGTCAATCTGAGCTTCCAGAGAGAGAAAAAGAGAAATGAGAAACAGTTAAAGTGT 2340  
Qy 2341 CTAATTAATGAG 2400  
Db 2341 CTAATTAATGAG 2400  
Qy 2401 AAAAGATCTGTAGAGAGTAGAGATTTTCACTGAGTACCTGATGATTAAGGCACTCAG 2460  
Db 2401 AAAAGATCTGTAGAGAGTAGAGATTTTCACTGAGTACCTGATGATTAAGGCACTCAG 2460  
Qy 2461 AAAAGATCTGTAGAGAGTAGAGATTTTCACTGAGTACCTGATGATTAAGGCACTCAG 2520  
Db 2461 AAAAGATCTGTAGAGAGTAGAGATTTTCACTGAGTACCTGATGATTAAGGCACTCAG 2520  
Qy 2521 GTGTGAGTCAAGTGTGAG 2580  
Db 2521 GTGTGAGTCAAGTGTGAG 2580  
Qy 2581 AATAATAGAAATGAGACAGAAAGGCTTTAATGATTCATGAGGAGCATGAGTAAACCAAGTC 2640  
Db 2581 AATAATAGAAATGAGACAGAAAGGCTTTAATGATTCATGAGGAGCATGAGTAAACCAAGTC 2640  
Qy 2641 GGGAAACAGCATGAGAAATGAGAAAGTGAATCTGATGCTCAATTTGAGAGATACAT 2700  
Db 2641 GGGAAACAGCATGAGAAATGAGAAAGTGAATCTGATGCTCAATTTGAGAGATACAT 2700  
Qy 2701 TCAAGGTTTCAAGGCGCAGTCACTTGTGCTGTTTCAAAATCCAGGAAATCCAGAAAGG 2760  
Db 2701 TCAAGGTTTCAAGGCGCAGTCACTTGTGCTGTTTCAAAATCCAGGAAATCCAGAAAGG 2760  
Qy 2761 AATGTGCAACATTTCTGCGCACTCTGGGCTCTTAAGAAACAAAGTCCAAAGTCACTT 2820  
Db 2761 AATGTGCAACATTTCTGCGCACTCTGGGCTCTTAAGAAACAAAGTCCAAAGTCACTT 2820  
Qy 2821 TTGAATGTGAACAAAGAGAGAAATCAAGAAAGATGAGTCTAATATCAAGCTGTAC 2880  
Db 2821 TTGAATGTGAACAAAGAGAGAAATCAAGAAAGATGAGTCTAATATCAAGCTGTAC 2880  
Qy 2881 AGACAGTTAATATGACAGTGGGCTTCTGCTGTTGTCAGAAAGATTAAGCAGTTGATA 2940  
Db 2881 AGACAGTTAATATGACAGTGGGCTTCTGCTGTTGTCAGAAAGATTAAGCAGTTGATA 2940  
Qy 2941 ATGCAATATGATATGACAGTGGGCTTCTGCTGTTGTCAGAAAGATTAAGCAGTTGATA 3000  
Db 2941 ATGCAATATGATATGACAGTGGGCTTCTGCTGTTGTCAGAAAGATTAAGCAGTTGATA 3000  
Qy 3001 ACGAAACTGAGCTCATTAATCTCAAAATGAGAAATGAGAAATGAGAAATGAGAAAT 3060  
Db 3001 ACGAAACTGAGCTCATTAATCTCAAAATGAGAAATGAGAAATGAGAAATGAGAAAT 3060  
Qy 3061 CACCACTTTTCCATCAAGCTATTTGTTAAATGAGAAATGAGAAATGAGAAATGAGAA 3120  
Db 3061 CACCACTTTTCCATCAAGCTATTTGTTAAATGAGAAATGAGAAATGAGAAATGAGAA 3120  
Qy 3121 AAAACTTTGAGAAACATTTCAATGACCTGAGAAAGAGAAATGAGAAATGAGAAATGAG 3180  
Db 3121 AAAACTTTGAGAAACATTTCAATGACCTGAGAAAGAGAAATGAGAAATGAGAAATGAG 3180  
Qy 3181 GTACAGTGAAGCAATTAAGCCTTAATTAACATTAAGAGAAATGTTTTTAAAGAGCCAGCT 3240  
Db 3181 GTACAGTGAAGCAATTAAGCCTTAATTAACATTAAGAGAAATGTTTTTAAAGAGCCAGCT 3240

OY	3241	CAAGCAATATTAACAACTAGTCTCCATTACTAATGAATGGGCTCCAGTATTAATGAA	33000
Db	3241	CAAGCAATATTAATGAAGTAGGCTCCATTAAGAAATGGGCTCCAGTATTAATGAA	33000
OY	3301	TAGGTTCCAGTGAATGAACAATTCAAGAGAACTAGGTGAAGAAACAGAGGGCCAAAATTGA	33660
Db	3301	TAGGTTCCAGTGAATGAACAATTCAAGAGAACTAGGTGAAGAAACAGAGGGCCAAAATTGA	33660
OY	3361	ATGCTATGCTTAGATTTAGGGGTTTTTGCAACCTGAGGTATATMAACAAAGCTTCTGGAA	34200
Db	3361	ATGCTATGCTTAGATTTAGGGGTTTTTGCAACCTGAGGTATATMAACAAAGCTTCTGGAA	34200
OY	3421	GTAATGTAGACATCTCTGAATATAAAAAGCAAGATATGAAGAGTACTGACACTGTA	34800
Db	3421	GTAATGTAGACATCTCTGAATATAAAAAGCAAGATATGAAGAGTACTGACACTGTA	34800
OY	3481	ATACAGATTTCTCTCATATCTGATTTAGATTAATTGAACAGCTATGGGAAGTAGTC	35400
Db	3481	ATACAGATTTCTCTCATATCTGATTTAGATTAATTGAACAGCTATGGGAAGTAGTC	35400
OY	3541	ATGCATCTCAGGTTTGTCTGAGACACCTGATGACCTGTAGATGATGGTGAATTAAGG	36000
Db	3541	ATGCATCTCAGGTTTGTCTGAGACACCTGATGACCTGTAGATGATGGTGAATTAAGG	36000
OY	3601	AAGATACTAGTTTTCTGTAATAATGACATTAAGAAAGTTCTGCTGTTTTAGCAAAACCG	36600
Db	3601	AAGATACTAGTTTTCTGTAATAATGACATTAAGAAAGTTCTGCTGTTTTAGCAAAACCG	36600
OY	3661	TCCAGAGAGAGAGCTTGAACAGAGATCCTAGCCCTTACACCATACATTTGGCTCAGG	37200
Db	3661	TCCAGAGAGAGAGCTTGAACAGAGATCCTAGCCCTTACACCATACATTTGGCTCAGG	37200
OY	3721	GTTACCGAAGAGGGGCCCAAGAAATTAGAGTCTCTGAAAGAGAACTTATCTAGTAGATG	37800
Db	3721	GTTACCGAAGAGGGGCCCAAGAAATTAGAGTCTCTGAAAGAGAACTTATCTAGTAGATG	37800
OY	3781	AAGAGCTTCCGCTTCCACACTTGTAATTTGGTAAGTAACATATATACCTTCTCAGT	38400
Db	3781	AAGAGCTTCCGCTTCCACACTTGTAATTTGGTAAGTAACATATATACCTTCTCAGT	38400
OY	3841	CTACTAGGCATATGACACCGTTGCTACCGAGTGTCTGTATGAACACACAGAGAAATTAAT	39000
Db	3841	CTACTAGGCATATGACACCGTTGCTACCGAGTGTCTGTATGAACACACAGAGAAATTAAT	39000
OY	3901	TATCATTTGAAGATATGCTTTAAATGACTGACAGTAACAGAGTAATATTTGGCAAGGACATTC	39660
Db	3901	TATCATTTGAAGATATGCTTTAAATGACTGACAGTAACAGAGTAATATTTGGCAAGGACATTC	39660
OY	3961	AGGAACATCACCTTAGTAGAGGAACAAATGTTCTGCTAGCTGTGTTTTCTTCAAGTGCA	40200
Db	3961	AGGAACATCACCTTAGTAGAGGAACAAATGTTCTGCTAGCTGTGTTTTCTTCAAGTGCA	40200
OY	4021	GTGAATTTGGAAGACTTGAATCTGAAATACAAACACCCAGAGATCTTCTTGAATGGTTCTT	40800
Db	4021	GTGAATTTGGAAGACTTGAATCTGAAATACAAACACCCAGAGATCTTCTTGAATGGTTCTT	40800
OY	4081	CCAAACAATGAGGACATGCTGTAAGACGAGGAGTTGGTCTGAGTACAAGAAATTTGG	41400
Db	4081	CCAAACAATGAGGACATGCTGTAAGACGAGGAGTTGGTCTGAGTACAAGAAATTTGG	41400
OY	4141	TTTCAGATGATGAAGAAAGAGAACGGGCTTGGAGAAATATATCAAGAGGCAACACA	42000
Db	4141	TTTCAGATGATGAAGAAAGAGAACGGGCTTGGAGAAATATATCAAGAGGCAACACA	42000
OY	4201	TGGATTTCAAATTAGGTGAAGAGACATCTGGGTGTGAAGTGAACAAAGCCTCTCTGAAG	42600
Db	4201	TGGATTTCAAATTAGGTGAAGAGACATCTGGGTGTGAAGTGAACAAAGCCTCTCTGAAG	42600
OY	4261	ACTGCTCAGGGGCTATCTCTCAGAGTGAATTTTAACACCTCAGCAGAGGGGATACCATG	43200
Db	4261	ACTGCTCAGGGGCTATCTCTCAGAGTGAATTTTAACACCTCAGCAGAGGGGATACCATG	43200
OY	4321	AACATTAACCTGATTAAGCTCCAGCAGGAATGGCTGAATGAAAGACTGTGTAGAACG	43800

Db	4321	AACTAACTCTATTAAGCTCCAGAGGAATGSGTAACTGAAGCTGTGTAAACAGC	4380
Qy	4381	ATGGAGGCAACCTCTTAAACAGCTAACCTTCATCATTAAGTACCTCCTCGGTAAGG	4440
Db	4381	ATGGAGGCAACCTCTTAAACAGCTAACCTTCATCATTAAGTACCTCCTCGGTAAGG	4440
Qy	4441	ACCTGCGAATTCAGAACAAAGCAATCAAGAAAAAGCAGTATTAACTTCAAGAAAAGTA	4500
Db	4441	ACCTGCGAATTCAGAACAAAGCAATCAAGAAAAAGCAGTATTAACTTCAAGAAAAGTA	4500
Qy	4501	GTGAATTAACCCATTAAGCCAGAAATCAGAAAGGCCCTTTCGCTGACAAAGTTTAAAGGTCTG	4560
Db	4501	GTGAATTAACCCATTAAGCCAGAAATCAGAAAGGCCCTTTCGCTGACAAAGTTTAAAGGTCTG	4560
Qy	4561	CAGATAGTTCACAGATTAATAATAAAGAACAGAGTGAAGATTCATCCCTCTAAAT	4620
Db	4561	CAGATAGTTCACAGATTAATAATAAAGAACAGAGTGAAGATTCATCCCTCTAAAT	4620
Qy	4621	GCCCATCATTAAGATGATAGTGTGTCATGCAAGTTCCTGCGAGTCTTCAGAAATAGAA	4680
Db	4621	GCCCATCATTAAGATGATAGTGTGTCATGCAAGTTCCTGCGAGTCTTCAGAAATAGAA	4680
Qy	4681	ACTAACCTCTCAAGAGAGCTCATTTAAGTTGTGTAATGTGGAAGAGCAACGCTGGAG	4740
Db	4681	ACTAACCTCTCAAGAGAGCTCATTTAAGTTGTGTAATGTGGAAGAGCAACGCTGGAG	4740
Qy	4741	AGTCGGGCCACAGATTTGACGGAAACATCTTACCTTGCCAAAGCAAGATCTAAGGGAA	4800
Db	4741	AGTCGGGCCACAGATTTGACGGAAACATCTTACCTTGCCAAAGCAAGATCTAAGGGAA	4800
Qy	4801	CCCTTACCTTGAATCTGGAATCAGCCCTTCTCTGATGACCTTGAATCTGATCCTTCTG	4860
Db	4801	CCCTTACCTTGAATCTGGAATCAGCCCTTCTCTGATGACCTTGAATCTGATCCTTCTG	4860
Qy	4861	AAGACAGAGCCCCAGAGTCAAGCTGTGTGTGGCAACATACCATTTCAACCTCTGCAATGA	4920
Db	4861	AAGACAGAGCCCCAGAGTCAAGCTGTGTGTGGCAACATACCATTTCAACCTCTGCAATGA	4920
Qy	4921	AAGTTCCTTGAAGTTGACAGATTCGCGAGGGGTCAGCTGCTGATCTAATCTG	4980
Db	4921	AAGTTCCTTGAAGTTGACAGATTCGCGAGGGGTCAGCTGCTGATCTAATCTG	4980
Qy	4981	ATACTGCTGGTATTAATGCAATGGAAGAAAGTGAGCAGGAGAGCAGAAATTGACAG	5040
Db	4981	ATACTGCTGGTATTAATGCAATGGAAGAAAGTGAGCAGGAGAGCAGAAATTGACAG	5040
Qy	5041	CTTCAACAGAAAGGCTCAACAAAGATGTCATGCTGTGCTCGGCTGACCCAGAG	5100
Db	5041	CTTCAACAGAAAGGCTCAACAAAGATGTCATGCTGTGCTCGGCTGACCCAGAG	5100
Qy	5101	AATTATGCTGTGTAACAAGTTCCGAGAAACACCAATCACTTAACTTAATCTTAATTA	5160
Db	5101	AATTATGCTGTGTAACAAGTTCCGAGAAACACCAATCACTTAACTTAATCTTAATTA	5160
Qy	5161	CTGAAGAGACTCACTGTTGTATGAAGAACAGATGCTGATTTGTGTGAACGACAC	5220
Db	5161	CTGAAGAGACTCACTGTTGTATGAAGAACAGATGCTGATTTGTGTGAACGACAC	5220
Qy	5221	TGAAATATTTCTAGAAATGCGGAGGAAATGGGTAAGTTAGTATTTCTGGGTGACCC	5280
Db	5221	TGAAATATTTCTAGAAATGCGGAGGAAATGGGTAAGTTAGTATTTCTGGGTGACCC	5280
Qy	5281	AGCTATTTAAAGAAAGAAATATGCTGAATGAGCATATTTTGAAGTCAAGAGAAATGGG	5340
Db	5281	AGCTATTTAAAGAAAGAAATATGCTGAATGAGCATATTTTGAAGTCAAGAGAAATGGG	5340
Qy	5341	TCAATGGAAGAAACCAACAGAGTCCAAAGCAGAGAAAGAAATCCAGGACAGAAAGATCT	5400
Db	5341	TCAATGGAAGAAACCAACAGAGTCCAAAGCAGAGAAAGAAATCCAGGACAGAAAGATCT	5400
Qy	5401	TCAGGGGCTAGAAATCTGTGCTATAGGCCCTTCAACCAATGCCACAGATCAATCGG	5460
Db	5401	TCAGGGGCTAGAAATCTGTGCTATAGGCCCTTCAACCAATGCCACAGATCAATCGG	5460

Db 5401 TCAGGGGGCTAGAAATCTGTTGCTATGAGCCCTTCACCAACATGCCACAGATCAACTG 5460  
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Db 5461 AATGATGATGACAGTGTGTGCTTCTGTGTGTAAGAGCTTCATCACTACCTTG 5520  
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Db 5521 GCACAGGTGTCACCAATTTGTGTGTGTCAGCCAGATGCTGACAGAGCAATGAGCT 5580  
Qy 5581 TCCATGCAATTTGGCAGATGTGTGAGGCACTGTGTGTAACCCGAGAGTGGTGTGACA 5640  
Db 5581 TCCATGCAATTTGGCAGATGTGTGAGGCACTGTGTGTAACCCGAGAGTGGTGTGACA 5640  
Qy 5641 GTGTGACCTCTACAGGCGCAGAGCTGACACCTACTGATACCCAGATCCCCCA 5700  
Db 5641 GTGTGACCTCTACAGGCGCAGAGCTGACACCTACTGATACCCAGATCCCCCA 5700  
Qy 5701 GCCACTACTGA 5711  
Db 5701 GCCACTACTGA 5711

## RESULT 7

US-09-982-828-5  
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Publication No. US20030022184A1

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APPLICANT: Murphy, Patricia D.  
Allen, Antoinette C.  
Alvares, Christopher P.  
Critz, Brenda S.  
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Thunder, Denise  
Zeng, Bin  
TITLE OF INVENTION: Coding Sequences of the Human  
BRCA1 Gene  
NUMBER OF SEQUENCES: 72  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Morgan Lewis & Bockius LLP  
STREET: 1111 Pennsylvania Avenue N. W.  
CITY: Washington  
STATE: DC  
COUNTRY: USA  
ZIP: 20004

## COMPUTER READABLE FORM:

COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/982,828  
FILING DATE: 22-Oct-2001  
CLASSIFICATION: <unknown>

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APPLICATION NUMBER: US 09/074,453  
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FILING DATE: 1996-02-12

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REFERENCE/DOCKET NUMBER: 44921-5053-01-US  
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## INFORMATION FOR SEQ ID NO: 5:

SEQUENCE CHARACTERISTICS:  
LENGTH: 5711 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: not relevant

TOPOLOGY: linear  
MOLECULE TYPE: cDNA  
ORIGINAL SOURCE:  
ORGANISM: Homo sapiens  
STRAIN: BRCA1 (om13)  
POSITION IN GENOME:  
CHROMOSOME/SEGMENT: 17  
MAP POSITION: 17q21  
SEQUENCE DESCRIPTION: SEQ ID NO: 5:  
US-09-982-828-5

Query Match 99.8%; Score 5701.4; DB 11; Length 5711;  
Best Local Similarity 99.9%; Pred. No. 0;  
Matches 5705; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

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Db 1 AGCTGCTGAGACTTCTCTGAGACCCGCAACAGAGCTGTGGGTTTCTAGATTAAGTGGCC 60  
Qy 61 CTTGGGCTCAGAGAGCCCTTACCCCTGCTGTGGTAAAGTTCAATGGAAACAGAAAGAA 120  
Db 61 CTTGGGCTCAGAGAGCCCTTACCCCTGCTGTGGTAAAGTTCAATGGAAACAGAAAGAA 120  
Qy 121 TGGATTTATCTGCTCTTGGGTTGAGAGATCAAAATGTCATTATGCTATGAGAGAAA 180  
Db 121 TGGATTTATCTGCTCTTGGGTTGAGAGATCAAAATGTCATTATGCTATGAGAGAAA 180  
Qy 181 TCTTAGAGTGTCCATGTGTGTGAGTTGATCAAGAACTGTCTCAACAAAGTGTACC 240  
Db 181 TCTTAGAGTGTCCATGTGTGTGAGTTGATCAAGAACTGTCTCAACAAAGTGTACC 240  
Qy 241 ACATATTTTGCAATTTTGATGCTGAACTCTCAACAGAAAGAGGCTTCAAGT 300  
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Db 361 AACTGTTGAAGAGCTATTTGAATCAATTTGTGCTTTTCAAGTTGACAGAGTTGGAGT 420  
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Db 481 AAGTTCTATCATCAAAAGATAGGCTACAGAAACGCTGCAAAAGACTTCAAGAGTG 540  
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Db 541 AACCCGAAATCTCTCTTCTGAGAGAAACAGTCTCAGTGTCCAACTCTTAACCTTGGAA 600  
Qy 601 CTGGAAGACTCTGAGAGCAAGAGGATACCACTCAAAAGACTGTCTACACTTG 660  
Db 601 CTGGAAGACTCTGAGAGCAAGAGGATACCACTCAAAAGACTGTCTACACTTG 660  
Qy 661 AATTGGATCTGATTTCTTCTGAGATACCGTTATTAAGCACTTAATGAGAGTGGAG 720  
Db 661 AATTGGATCTGATTTCTTCTGAGATACCGTTATTAAGCACTTAATGAGAGTGGAG 720  
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Db 721 ATCAAGATTTGTAACAAATACCCCTCAAGAAACAGAGGATGAATCAGTTGGATTCTG 780  
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Db 781 CAAAAAGGCTGCTGTAATTTTCTGAGACGATGTAACAAATCTGAACATCAAC 840  
Qy 841 CCAGTAATATGATTTGAACACCACTGAGAGGCTGAGGCAATCCAGAAAGT 900  
Db 841 CCAGTAATATGATTTGAACACCACTGAGAGGCTGAGGCAATCCAGAAAGT 900



Db 841 CCAGTAATATGATTTGGAACAACCTGGAAGCGTGACGTGAGAGCATCCAGAAAAGT 900  
Qy ATCAGGGATGTTCTGTTCAAACTTGATGATGAGACCATGAGCAAAATCTCATGCA 960  
Db ATCAGGGATGTTCTGTTCAAACTTGATGAGACCATGAGCAAAATCTCATGCA 960  
Qy 961 GCTCATTCAGCATGAGAACAGCAGTTTATTACTCATTAAGACAGAAATGATGAGAA 1020  
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Qy 1021 AGCGTGAATTTCTGATATTAAGCAAAACAGCTGCTGATGAGAGGCAACATTAACAGAT 1080  
Db 1021 AGCGTGAATTTCTGATATTAAGCAAAACAGCTGCTGATGAGAGGCAACATTAACAGAT 1080  
Qy 1081 GGGCTGGAAGTAAAGAAACATGATATGATAGGCGGACCTCCAGCAACAGAAAAAGGTAG 1140  
Db 1081 GGGCTGGAAGTAAAGAAACATGATATGATAGGCGGACCTCCAGCAACAGAAAAAGGTAG 1140  
Qy 1141 ATCTGAATGCTGATCCCTGTGTGAGAGAAAAAGATGAAATGAGCAAACTGCGATGCT 1200  
Db 1141 ATCTGAATGCTGATCCCTGTGTGAGAGAAAAAGATGAAATGAGCAAACTGCGATGCT 1200  
Qy 1201 CAGAGAACTCTAGAGATATCTGAAGATGTTCTTGATTAACATAATAGCAGCATTTCA 1260  
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Db 1501 TTGGGAAAACTATGGAAGAAAGGCAAGCTTCCCACTTAAAGCAATGTAATTC 1560  
Qy 1561 TAAATTAAGAGCAATTTGTTACTGAGCAAGATTAATCAAGAGGCTCCCTCAGAAATA 1620  
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Qy 1621 AATTAAAGCGTAAAGAGAGCACTACATGAGGCTTCATCTGAGGATTTTATCAAGAAAG 1680  
Db 1621 AATTAAAGCGTAAAGAGAGCACTACATGAGGCTTCATCTGAGGATTTTATCAAGAAAG 1680  
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Qy 1741 AGAATGCTCAAGTGAATATTAATTAATGATGATGATGATGATGATGATGATGATG 1800  
Db 1741 AGAATGCTCAAGTGAATATTAATTAATGATGATGATGATGATGATGATGATGATG 1800  
Qy 1801 CTATTCAGATGAGAAAAATCTTAACCAATGAAATCACTGGAAGAAATCTGCTTTCA 1860  
Db 1801 CTATTCAGATGAGAAAAATCTTAACCAATGAAATCACTGGAAGAAATCTGCTTTCA 1860  
Qy 1861 AAAAGCAAGCTGAACCTTAAGCAAGCAATTAATGAAATTAATGAAATTAATTAATTC 1920  
Db 1861 AAAAGCAAGCTGAACCTTAAGCAAGCAATTAATGAAATTAATGAAATTAATTAATTC 1920  
Qy 1921 ACAATTCAGAAAGCACTTAAGCAAGCAATTAATGAAATTAATGAAATTAATTAATTC 1980  
Db 1921 ACAATTCAGAAAGCACTTAAGCAAGCAATTAATGAAATTAATGAAATTAATTAATTC 1980

Qy 1981 ATGCGCTTGAACCTAGTACTAGTGAATCTTAAGCCCACTTAATTTGATCTGAATTCGAAA 2040  
Db 1981 ATGCGCTTGAACCTAGTACTAGTGAATCTTAAGCCCACTTAATTTGATCTGAATTCGAAA 2040  
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Db 2401 AAAAGTCTGTAAGAGTGAAGTATTTCACTGATGATGATGATGATGATGATGATGATG 2460  
Qy 2461 AAAAGTCTGTAAGAGTGAAGTATTTCACTGATGATGATGATGATGATGATGATGATG 2520  
Db 2461 AAAAGTCTGTAAGAGTGAAGTATTTCACTGATGATGATGATGATGATGATGATGATG 2520  
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Db 2521 GTGTGAGTCAAGTGAAGCAATTTGAAAAACCCCAAGGCACTTAATTCATGTTTCCAAAG 2580  
Qy 2581 ATTAATGAAATGACACAGAAAGCTTTAATGATGATGATGATGATGATGATGATGATG 2640  
Db 2581 ATTAATGAAATGACACAGAAAGCTTTAATGATGATGATGATGATGATGATGATGATG 2640  
Qy 2641 GGGAAACAAAGCATGAAATGAAAGTGAATGATGATGATGATGATGATGATGATGATG 2700  
Db 2641 GGGAAACAAAGCATGAAATGAAAGTGAATGATGATGATGATGATGATGATGATGATG 2700  
Qy 2701 TCAAGTTTCAAGGCGCCAGTCTTGTCTGTTTCAATCCAGAAATCCAGAAAGG 2760  
Db 2701 TCAAGTTTCAAGGCGCCAGTCTTGTCTGTTTCAATCCAGAAATCCAGAAAGG 2760  
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Qy 2821 TTGAATGTGAACAAAGAGAAATCAAGAAAGATGATGATGATGATGATGATGATGATG 2880  
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Qy 2941 ATGCAAAATGATATCAAGAGGCTTCTGTGTTGCTCAGAAAGATTAAGCAGTTGATA 3000  
Db 2941 ATGCAAAATGATATCAAGAGGCTTCTGTGTTGCTCAGAAAGATTAAGCAGTTGATA 3000  
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Db 3001 ACAGAACTGACATTAATCTCAATTAACATGATGATGATGATGATGATGATGATGATG 3060

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Db 3061 CACCACTTTTCCCATCAAGTCATTTGTTAAACTAATGTAGAAGAAATCTGCTAGAGG 3120  
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Db 3121 AAAACTTTGAGGAAACATTCATGTCACTGAAAAGAAAATGGAAATAGAACATTTCCA 3180  
QY 3181 GTACGCTAGGACCAATTTAGCCCTTAATCACTTAGGAAAATGTTTTTAAAGAGCCAGCT 3240  
| | | | |  
Db 3181 GTACGCTAGGACCAATTTAGCCCTTAATCACTTAGGAAAATGTTTTTAAAGAGCCAGCT 3240  
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Db 3241 CAAGCAATATTAATGAAGTAGGTTCCAGTAATAAGAGTGGGCTCCAGTATTAATGAAA 3300  
QY 3301 TAGGTTCCAGTGATGAAAACATTCAGACGAACTAGTAGAAAACAGAGGCCAAATTTGA 3360  
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QY 3361 ATGCTATGCTTAGATTAAGGGGTTTGGCACTGAGAGTCTATTAACAAAGCTTCTTGAA 3420  
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Db 3361 ATGCTATGCTTAGATTAAGGGGTTTGGCACTGAGAGTCTATTAACAAAGCTTCTTGAA 3420  
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Db 3421 GTAATTGTAGCATCTGTAATAATAAAGCAAGAAATAGAGAAAGTAGTTCAGACTGTTA 3480  
QY 3481 ATACAGATTTTCTCTCAATATCTGATTTCAATTAAGAACAGCTTAATGGAGATAGTC 3540  
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Db 3481 ATACAGATTTTCTCTCAATATCTGATTTCAATTAAGAACAGCTTAATGGAGATAGTC 3540  
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Db 3541 ATGCTATCAGGTTTGTCTGAGACACCTGATGACCTGTTAGATAGTAGTGAATAAAG 3600  
QY 3601 AAGATATAGTTTGTCTGAAAATGAATTAAGGAAAGTCTGCTGTTTGTAGCAAAACG 3660  
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Db 3601 AAGATATAGTTTGTCTGAAAATGAATTAAGGAAAGTCTGCTGTTTGTAGCAAAACG 3660  
QY 3661 TCCAGAGGAGAGCTTAGCAGAGTCTAGCCCTTTCACCATACACATTTGGCTCAGG 3720  
| | | | |  
Db 3661 TCCAGAGGAGAGCTTAGCAGAGTCTAGCCCTTTCACCATACACATTTGGCTCAGG 3720  
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| | | | |  
Db 3721 GTTACCAAGAGGGGSCAAGAAATTAGATCCTCAAGAGAACCTTACTAGTAGAGAG 3780  
QY 3781 AAGAGCTTCCCTGCTTCCAACTTTGTAATTTGTAAAGTAAACAATATACCTTCTCAGT 3840  
| | | | |  
Db 3781 AAGAGCTTCCCTGCTTCCAACTTTGTAATTTGTAAAGTAAACAATATATCTTCTCAGT 3840  
QY 3841 CTACTAGGCAATAGCACCTGTTGCTACGAGTCTGTCTTAAGAACACAGAGAGAAATTAAT 3900  
| | | | |  
Db 3841 CTACTAGGCAATAGCACCTGTTGCTACGAGTCTGTCTTAAGAACACAGAGAGAAATTAAT 3900  
QY 3901 TATCATTTGAAGAAATAGCTTAATGACCTGAGTAACAGAGTAATTTGGCAAAAGCATCTC 3960  
| | | | |  
Db 3901 TATCATTTGAAGAAATAGCTTAATGACCTGAGTAACAGAGTAATTTGGCAAAAGCATCTC 3960  
QY 3961 AGGAAACATCACCTTAGTAGAGAAACAAATATGTTCTGCTAGCTTGTCTTCAAGTCA 4020  
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Db 3961 AGGAAACATCACCTTAGTAGAGAAACAAATATGTTCTGCTAGCTTGTCTTCAAGTCA 4020  
QY 4021 GTGAATTGGAAGACTTGACTGCAAAATACAAACCCAGAGATCTTTCTTGATGGTCTT 4080  
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Db 4021 GTGAATTGGAAGACTTGACTGCAAAATACAAACCCAGAGATCTTTCTTGATGGTCTT 4080  
QY 4081 CCAAAACAATAGAGCATAGTCTGAAAGCCAGAGAGTGTGTCTAGTAGAACAGAAATTTGG 4140  
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Db 4081 CCAAAACAATAGAGCATAGTCTGAAAGCCAGAGAGTGTGTCTAGTAGAACAGAAATTTGG 4140  
QY 4141 TTTGATGATGAGAAAGAGAAACGGGCTTGGAAAGAAATATCAAGAGAGCA 4200  
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Db 4141 TTTGATGATGAGAAAGAGAAACGGGCTTGGAAAGAAATATCAAGAGAGCA 4200  
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QY 4201 TGAATTCAACTTAGGTGAAGACAGATCTGGGTGAGAGTGAACAAAGCCTCTCTGAG 4260  
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Db 4201 TGAATTCAACTTAGGTGAAGACAGATCTGGGTGAGAGTGAACAAAGCCTCTCTGAG 4260  
QY 4261 ACTGCTCAGGGCTATCTCTCAGAGTGAATTTTAACTCAGACAGAGGATACATGC 4320  
| | | | |  
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| | | | |  
Db 4321 AACATTAACCTGATTAAGCTCCAGCAGAGAAATGGCTGAACCTGAAGCTGTGTAGAAC 4380  
QY 4381 ATGGAGCCAGCCTTCTTAACAGTACCTTCCATCATTAAGTGACTCTTCTGCTGAGG 4440  
| | | | |  
Db 4381 ATGGAGCCAGCCTTCTTAACAGTACCTTCCATCATTAAGTGACTCTTCTGCTGAGG 4440  
QY 4441 ACCTGGCAATCCAGAACAAAGCAATCAAGAAAAGCAATTTAACTTCAAGAAAAGTA 4500  
| | | | |  
Db 4441 ACCTGGCAATCCAGAACAAAGCAATCAAGAAAAGCAATTTAACTTCAAGAAAAGTA 4500  
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Db 4501 GTGAATACCTTATAGCCAGAACTCCAGAGGCTTTCTGCTGACAAAGTTGAGGTGCTG 4560  
QY 4561 CAGATAGTTCTTACGATTAATAAAGCAAGAGTGAAGTCAATCCCTTCTAAT 4620  
| | | | |  
Db 4561 CAGATAGTTCTTACGATTAATAAAGCAAGAGTGAAGTCAATCCCTTCTAAT 4620  
QY 4621 GCCCATCAATTAAGATAGTGTGATGACAGTGTCTGAGAGTCTTCAAGAAATGAA 4680  
| | | | |  
Db 4621 GCCCATCAATTAAGATAGTGTGATGACAGTGTCTGAGAGTCTTCAAGAAATGAA 4680  
QY 4681 ACTACCATCTCAAGAGAGCTCATTAAGGTTGTTGATGTGAGAGCAACAGCTGGAAG 4740  
| | | | |  
Db 4681 ACTACCATCTCAAGAGAGCTCATTAAGGTTGTTGATGTGAGAGCAACAGCTGGAAG 4740  
QY 4741 AGTCTGGGCCACAGATTTGACGAAACATCTTCAAGAGCAAGATCTAGAGGAA 4800  
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| | | | |  
Db 4801 CCCCTTACCTGGAATCTGGAATCAGCCTTCTCTGTGATGACCTGGAATCTGATCTCTG 4860  
QY 4861 AAGACAGAGCCCAAGAGTCAAGCTGTGTTGCAACATACATCTTCAACCTTGA 4920  
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Db 5161 CTGAAGAGACTACATGATTTGTTATGAAAACAGATGCTGAGTTTGTGTGAACGAGCAC 5220  
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Db 5221 TGAATATTTTCTGAGATTCGGAGAGAAATGGTAGTATTTCTGGTGACCC 5280  
Qy 5281 AGCTATTAAGAAGAAAAATGCTGATGAGCATGATTTGAGTACAGAGAGATGG 5340  
Db 5281 AGCTATTAAGAAGAAAAATGCTGATGAGCATGATTTGAGTACAGAGAGATGG 5340  
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Db 5401 TCAGAGGGGCTAGAAATCTGTTGCTATGAGGCCCTTACCAACATGCCAAGATCACTGG 5460  
Qy 5461 AATGGAATGCTACACTGTGTGTCTTCTGTGTGAAGAGACTTTCATCATTCACCTTG 5520  
Db 5461 AATGGAATGCTACACTGTGTGTCTTCTGTGTGAAGAGACTTTCATCATTCACCTTG 5520  
Qy 5521 GCACAGGTGTCACCCCAATTTGTTGTGACAGCAGATGCTTGACAGAGACAATGGCT 5580  
Db 5521 GCACAGGTGTCACCCCAATTTGTTGTGACAGCAGATGCTTGACAGAGACAATGGCT 5580  
Qy 5581 TCACATGCAATTTGGGCAAGATGTGTAGGCACTGTGTGTACCCGAGAGTGGGTGGACA 5640  
Db 5581 TCACATGCAATTTGGGCAAGATGTGTAGGCACTGTGTGTACCCGAGAGTGGGTGGACA 5640  
Qy 5641 GTGTAGCACTTACCAAGTCCAGAGCTGACACCTACTATACCCCAATCCCCCA 5700  
Db 5641 GTGTAGCACTTACCAAGTCCAGAGCTGACACCTACTATACCCCAATCCCCCA 5700  
Qy 5701 GCCACTACTGA 5711  
Db 5701 GCCACTACTGA 5711

RESULT 8  
US-10-240-965-268  
; Sequence 268, Application US/10240965  
; Publication No. US20030165924A1  
; GENERAL INFORMATION:  
; APPLICANT: INCYTE GENOMICS, INC.  
; APPLICANT: SHIFFMAN, DOV  
; APPLICANT: SOMOGYI, Roland  
; APPLICANT: LAWN, Richard M.  
; APPLICANT: SEILHAMER, Jeffrey J.  
; APPLICANT: PORTER, Gordon J.  
; APPLICANT: MIKITA, Thomas  
; APPLICANT: TAL, Julie  
; TITLE OF INVENTION: GENES EXPRESSED IN FOAM CELL DIFFERENTIATION  
; FILE REFERENCE: PA-0025 PCT  
; CURRENT APPLICATION NUMBER: US/10/240, 965  
; PRIOR FILING DATE: 2002-10-04  
; PRIOR APPLICATION NUMBER: 60/195,106  
; NUMBER OF SEQ ID NOS: 276  
; SOFTWARE: PERL Program  
; SEQ ID NO 268  
; LENGTH: 5709  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
; FEATURES:  
; NAME/KEY: misc feature  
; OTHER INFORMATION: incyte ID No. US20030165924A1 1098141.1  
US-10-240-965-268

Query Match 98.9%; Score 5649.8; DB 13; Length 5709;  
Best Local Similarity 99.8%; Pred. No. 0;  
Matches 5700; Conservative 0; Mismatches 7; Indels 6; Gaps 4;

Qy 1 AGCTGCTGAGACTTCTCTGACCCCGACCAAGCTGTGGGTTTCTCAGATPACTGGGCC 60  
Db 1 AGCTGCTGAGACTTCTCTGACCCCGACCAAGCTGTGGGTTTCTCAGATPACTGGGCC 60

Qy 61 CCTGCGCTCAGAGAGCCCTTCACCTCTGCTCTGGGTAAAGTTCAATGGAACAGAAAGAA 120  
Db 61 CCTGCGCTCAGAGAGCCCTTCACCTCTGCTCTGGGTAAAGTTCAATGGAACAGAAAGAA 120  
Qy 121 TGAATTAATCTCTCTTCTGCGGTGAAGAGTACAAAATGTCATTAATGCTATGCAAGAAA 180  
Db 121 TGAATTAATCTCTCTTCTGCGGTGAAGAGTACAAAATGTCATTAATGCTATGCAAGAAA 180  
Qy 181 TCTTAGAGTGTCCCATCTGTCTGAGTGTATCAAGGAACCTGTCTCCAAAGTGTGACC 240  
Db 181 TCTTAGAGTGTCCCATCTGTCTGAGTGTATCAAGGAACCTGTCTCCAAAGTGTGACC 240  
Qy 241 ACATATTTTGAAGATTTTGTGACGTGAAACTTCTCAACAGAGAAAGAGGCTTCACAGT 300  
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Qy 301 GTTCCTTAATGTAAGATGATTAACCAAAAGAGCCTTACAAAGAGTACGAGATTTAGTC 360  
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Qy 361 AACTTTGTAAGAGCTATGGAATATCTTTGTGCTTTTACGCTTGAACACAGTTTGGAGT 420  
Db 361 AACTTTGTAAGAGCTATGGAATATCTTTGTGCTTTTACGCTTGAACACAGTTTGGAGT 420  
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Db 421 ATGCAAAAGCTTAATTTTTCGCAAAAAGAAATTAATCTCTGAAACATCTAAAGATG 480  
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Db 541 AACCAGAAATCTCTCTCTGAGAGAAACCACTCAAGTGTCAACTCTTAACCTTGGAA 600  
Qy 601 CTGTGAGAACTCTGAGGACAAAGCAGGAGTACAACTCAAAAGAGCTCTGTACATTTG 660  
Db 601 CTGTGAGAACTCTGAGGACAAAGCAGGAGTACAACTCAAAAGAGCTCTGTACATTTG 660  
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Db 661 AATGGAGATCTGATTTCTTCTGAAAGTACCGTTAATTAAGCAATTAATGCGATGGAG 720  
Qy 721 ATCAAGAAATTTTCAAAATCACCCCTCAAGGACCAAGGATGAATCACTTTGATTTG 780  
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Qy 781 CAAAAAGGCTGTGGAATTTCTGAGACGATGTGAACAAATGCAATCATCATCAAC 840  
Db 781 CAAAAAGGCTGTGGAATTTCTGAGACGATGTGAACAAATGCAATCATCATCAAC 840  
Qy 841 CCAGTAATTAATGATTTTGAACACACTGAGAGCGTGTGAGAGGATCCAGAAAAAGT 900  
Db 841 CCAGTAATTAATGATTTTGAACACACTGAGAGCGTGTGAGAGGATCCAGAAAAAGT 900  
Qy 901 ATCAAGGATGTTCTGTTTCAAACTTGCAATGTGAGCCATGTGGCAAAATCTCATGCCA 960  
Db 901 ATCAAGGATGTTCTGTTTCAAACTTGCAATGTGAGCCATGTGGCAAAATCTCATGCCA 960  
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Db 1021 AGGCTGAATTTCTGTAATTAAGCAAAAGAGCTGTGCTTGAAGAGGCCACATTAACAGAT 1080  
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Db 1081 GGGCTGGAAGTAAAGAAACATGTATATGATGAGCGGATCTCCAGACACAGAAAAAGGTG 1140  
Qy 1141 ATCTGAATGCTGATCCCTGTGTGAGAGAAAGATGAATTAACAGAAATCGCATGCT 1200

Db 1141 ATCTGAATGCTGATCCCTGTGTGAGAGAAAAGATGAAATAGAGCAAAACCTGCCATCT 1200  
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Db 1201 CAGAGAAATCTTGAATACTGAAGATGTTCTTGGATTAACCTAAATAGCGACATTGAGA 1260  
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Db 1261 AAGTTAATGAGTGTGTTTCCAGAGATGATGAACCTGTGGTTCTGATGACCTCACATGATG 1320  
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Db 1561 TAAATATGAGAGCATTGTTGTAATGAGCCACAGATTAATCAAGAGAGTCCCTCACAAATA 1620  
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Db 1621 AATTAAGCCTTAAGAGAGACCTACATCAGAGCTTCATCTGAGGATTTTATCAAGAAAG 1680  
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Qy 1741 AGAATGCTCAAGTGAATGAAATTTACTATATAGTGTCAATGAGAAATTAACAAAGATGATT 1800  
Db 1741 AGAATGCTCAAGTGAATGAAATTTACTAATATAGTGTCAATGAGAAATTAACAAAGATGATT 1800  
Qy 1801 CTATTCAGAAATGAGAAAAATCTTAACCAATAGATCACTCGAAAAAGAACTCTGTTTCA 1860  
Db 1801 CTATTCAGAAATGAGAAAAATCTTAACCAATAGATCACTCGAAAAAGAACTCTGTTTCA 1860  
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Db 1861 AAACGAAAGCTGAACCTTAAGCAGAGTATTAAGCAATATGGAATCTGGAATTAATATCC 1920  
Qy 1921 ACAATTCAAAAAGCACTTAAGAAAGAAATGAGGAGAGAGAGTCTTCAACGAGGATATTC 1980  
Db 1921 ACAATTCAAAAAGCACTTAAGAAAGAAATGAGGAGAGAGAGTCTTCAACGAGGATATTC 1980  
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Db 1981 ATGCGCTTGAATAGTAGTCAAGTAAATCTAAGCCCACTAATTTGACTGAATTTGCAAA 2040  
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Db 2041 TTGATAGTGTCTTACAGAGTGAAGATTAAGAAAAAAGTACAAACCAATGTCAGATCA 2100  
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Db 2101 GGCACAGAGAAACCTCAACTCAATGAGAGGTAAAGAACTGCAACCTGAGCCCAAGAGA 2160  
Qy 2161 GTAAACAAGCCAAATGAACAGACAGTAAAGACATGACAGTATCTTCCACAGAGCTGA 2220  
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QY 4437 ATGGAGAGCAGCTTTCTTAAGCTTACCTTTCATCATTAAGTACTCTCTGACCTTGA 4437

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Db 4498 TAGTGAATACCTTAATTAAGCAAGATCCAGAAAGCCTTTCTGCTGACAAAGTTTGAAGTGC 4557  
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Db 4678 AAACCTACCATCTCAGAGAGGCTCATTTAAGTTGTTGATGAGAGACAAAGCTTGA 4737  
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Db 4918 GAAAGTTCCCAATTGAAGTGAAGTGAAGATCTGCCAGAGTCTGCTCATATAC 4977  
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QY 5099 AGAATTTATGCTGCTGATCAAGTTTGCAGAAACACACATCACTTTAATCTAAT 5158  
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QY 5219 ACTGAATATTTTCTAGAAATGCGGAGAGAAATGGGTATGATTTCTGGGTGAC 5278  
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Db 5398 CTTGAGGGGCTGAGAAATCTGTTGCTATGGGCTTCAACCAATGCGCAGATCAACT 5457  
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Db 5458 GGAATGATGATGATACAGCTGTGTGCTTCTGTGTGAAGAG-TTTCATCATTAACCTT 5516  
QY 5519 TGGCAGAGGTGTCCACCAATTTGTGTGTGACCGAGATGCTCTGACAGAGCAATGG 5578





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Qy 2018 ACCTAATTTGACTGAATTTGCAATTTGATGTTCTTCTAGCAGTGAAGATTAAGAAAA 2077
Db 202 ACCTAATTTGACTGAATTTGCAATTTGATGTTCTTCTAGCAGTGAAGATTAAGAAAA 143
Qy 2078 AAGATCAACCAAAATGCGAGTCAAGCAGACAGAAAACTTCACTCATGAGGTAAGA 2137
Db 142 AAGATCAACCAAAATGCGAGTCAAGCAGACAGAAAACTTCACTCATGAGGTAAGA 83
Qy 2138 ACCTGCAACTGAGCCCAAGAGATTAACCAAGCCAAATTAACAGCAAGTAAAGACATGA 2197
Db 82 ACCTGCAACTGAGCCCAAGAGATTAACCAAGCCAAATTAACAGCAAGTAAAGACATGA 23
Qy 2198 CAGTGAATCTTTCCAGAGCTG 2219
Db 22 CAGGATTAATCTTTCCAGAGCTG 1

RESULT 11
US-10-029-386-2689/c
; Sequence 2689, Application US/10029386
; Publication No. US20030194704A1
; GENERAL INFORMATION:
; APPLICANT: Penn, Sharon G.
; APPLICANT: Rank, David R.
; APPLICANT: Hanzel, David K.
; TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR C
; FILE REFERENCE: AECOMICA-X-2
; CURRENT APPLICATION NUMBER: US/10/029,386
; CURRENT FILING DATE: 2001-12-20
; NUMBER OF SEQ ID NOS: 34288
; SOFTWARE: Annomax Sequence Listing Engine vers. 1.1
; SEQ ID NO 2689
; LENGTH: 505
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: MAP TO CHR17.1
; OTHER INFORMATION: EXPRESSED IN BRAIN, SIGNAL = 0.8
; OTHER INFORMATION: EXPRESSED IN ADULT LIVER, SIGNAL = 0.75
; OTHER INFORMATION: EXPRESSED IN HEART, SIGNAL = 0.85
; OTHER INFORMATION: EXPRESSED IN BONE MARROW, SIGNAL = 0.97
; OTHER INFORMATION: SWISSPROT HIT: P38398, EVALUE 2.00e-80
; OTHER INFORMATION: EST_HUMAN HIT: BE564528.1, EVALUE 0.00e+00
; OTHER INFORMATION: NT HIT: L78833.1, EVALUE 0.00e+00
; US-10-029-386-2689

Query Match 7.3%; Score 416; DB 13; Length 505;
Best Local Similarity 100.0%; Pred. No. 1.5e-96;
Matches 416; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 789 GCTCTGTGGAATTTTCTGAGACGGATGTAACTAATCTGAACATCATCAACCCAGTAT 848
Db 416 GCTCTGTGGAATTTTCTGAGACGGATGTAACTAATCTGAACATCATCAACCCAGTAT 357
Qy 849 AATGATTTGAACACCACTGAGAAAGCTGACGTGAGAGCCATCCGAAAAAGTATCAGGCT 908
Db 356 AATGATTTGAACACCACTGAGAAAGCTGACGTGAGAGCCATCCGAAAAAGTATCAGGCT 297
Qy 909 AGTCTGTTTCAAACTTGCATGTGGAGCCATGTGGCACTCAATATCTCATGCCAGCTCATTA 968
Db 296 AGTCTGTTTCAAACTTGCATGTGGAGCCATGTGGCACTCAATATCTCATGCCAGCTCATTA 237
Qy 969 CAGCATGAGAACAGCAGTTTATTACTCACTAAAGACAGATGATGTAGAAAGGCTGAA 1028
Db 236 CAGCATGAGAACAGCAGTTTATTACTCACTAAAGACAGATGATGTAGAAAGGCTGAA 177
Qy 1029 TTCTGTATTAAGAAAGCAAGCCTGCTTACGAGAGACCAATTAACAGTGGCTGGA 1088
Db 176 TTCTGTATTAAGAAAGCAAGCCTGCTTACGAGAGACCAATTAACAGTGGCTGGA 117
Qy 1089 AGTAAGAAACATGATGATGAGCGGAGCTCCACAGACAGAAAAAAGTGTGATCTGAT 1148
Db 1148 AGTAAGAAACATGATGATGAGCGGAGCTCCACAGACAGAAAAAAGTGTGATCTGAT 1148
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Db 116 AGTAAGAAACATGATGATGAGCGGAGCTCCACAGACAGAAAAAAGTGTGATCTGAT 57
Qy 1149 GCTATCCCTGCTGTGAGAGAAAGATTAAGAAATGAAGAACTGCATGCTGCA 1204
Db 56 GCTATCCCTGCTGTGAGAGAAAGATTAAGAAATGAAGAACTGCATGCTGCA 1

RESULT 12
US-09-911-904-127
; Sequence 127, Application US/09911904
; Publication No. US20030096234A1
; GENERAL INFORMATION:
; APPLICANT: Farr, Spencer B.
; APPLICANT: Pickett, Gavin G.
; APPLICANT: Neft, Robin Eileen
; APPLICANT: Dunn, II, Robert Thomas
; TITLE OF INVENTION: CANINE TOXICITY GENES
; FILE REFERENCE: 400742000200
; CURRENT APPLICATION NUMBER: US/09/911,904
; CURRENT FILING DATE: 2002-04-09
; PRIOR APPLICATION NUMBER: US 60/220,057
; PRIOR FILING DATE: 2000-07-21
; NUMBER OF SEQ ID NOS: 386
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 127
; LENGTH: 499
; TYPE: DNA
; ORGANISM: Canis familiaris
; US-09-911-904-127

Query Match 6.4%; Score 364.6; DB 11; Length 499;
Best Local Similarity 86.7%; Pred. No. 2.7e-83;
Matches 419; Conservative 0; Mismatches 49; Indels 15; Gaps 1;

Qy 5229 TTTCTAGGAATTTGCGGAGGAGAAATGGTATGTAATTTCTGCTGACCCAGTCTATT 5288
Db 1 TTTCTAGGAATTTGCGGAGGAGAAATGGTATGTAATTTCTGCTGACCCAGTCTATT 60
Qy 5289 AAGAAAGAAATGCTGAATGACATGATTTTGAAGTCAAGAGAGATGTGTCATGGA 5348
Db 61 AAGAAAGAAATGCTGAATGACATGATTTTGAAGTCAAGAGAGATGTGTCATGGA 120
Qy 5349 AGAAACCAACCAAGTCCAAAGCCGCAAGAGAAATCCAG-----GACAGA 5393
Db 121 AGAAATCAACCAAGTCCAAAGCCGCAAGAGAAATCCAGAAATCCAAAGACAGA 180
Qy 5394 AAGATCTTACAGGGGCTAGAAATCTGTTGCTATGAGCCCTTCAACCAATGCCACAGAT 5453
Db 181 AAGATCTTACAGGGGCTAGAAATCTGTTGCTATGAGCCCTTCAACCAATGCCACAGAT 240
Qy 5454 CAATGGAATGATGTGACAGCTGTGTGCTTCTGTGTGAAAGAGCTTTCATCATTC 5513
Db 241 CAATGGAATGATGTGACAGCTGTGTGCTTCTGTGTGAAAGAGCTTTCATCATTC 300
Qy 5514 ACCCTTGCAACAGGTGTCACCAATTTGTGTTGTGACCAAGATGCTTGACAGAGAC 5573
Db 301 ACCCTTGCAACAGGTGTCACCAATTTGTGTTGTGACCAAGATGCTTGACAGAGAC 360
Qy 5574 AATGCTTCCATGGAATTTGGGCAAGTGTGAGGCACTGTGTGAGACCCGAGAGTGGTG 5633
Db 361 AATGCTTCCATGGAATTTGGGCAAGTGTGAGGCACTGTGTGAGACCCGAGAGTGGTG 420
Qy 5634 TTGACAGTGTGAGCACTTCACTCAAGTCCAGAGCTGACACCTTACCTGATACCCAGATC 5693
Db 421 CTGACAGTGTGAGCACTTCACTCAAGTCCAGAGCTGACACCTTACCTGATACCCAGATC 480
Qy 5694 CCC 5696
Db 481 CCC 483

RESULT 13
US-10-029-386-16389/c
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; PRIOR APPLICATION NUMBER: PCT/US01/00661  
; PRIOR FILING DATE: 2001-01-30  
; PRIOR APPLICATION NUMBER: PCT/US01/00670  
; PRIOR FILING DATE: 2001-01-30  
; PRIOR APPLICATION NUMBER: US 60/234,687  
; PRIOR FILING DATE: 2000-09-21  
; PRIOR APPLICATION NUMBER: US 09/608,408  
; PRIOR FILING DATE: 2000-06-30  
; PRIOR APPLICATION NUMBER: US 09/774,203  
; PRIOR FILING DATE: 2001-01-29  
; NUMBER OF SEQ ID NOS: 49117  
; SOFTWARE: Anomax Sequence Listing Engine vers. 1.1  
; SEQ ID NO 4552  
; LENGTH: 424  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
; FEATURE:  
; OTHER INFORMATION: MAP TO L78833.1  
; OTHER INFORMATION: EXPRESSED IN FETAL LIVER, SIGNAL = 3.4  
; OTHER INFORMATION: EXPRESSED IN ADULT LIVER, SIGNAL = 1.7  
; OTHER INFORMATION: EXPRESSED IN LUNG, SIGNAL = 2  
; OTHER INFORMATION: EXPRESSED IN BONE MARROW, SIGNAL = 2.1  
; OTHER INFORMATION: EXPRESSED IN BRAIN, SIGNAL = 2.3  
; OTHER INFORMATION: EXPRESSED IN PLACENTA, SIGNAL = 2  
; OTHER INFORMATION: EXPRESSED IN BT474, SIGNAL = 1.9  
; OTHER INFORMATION: EXPRESSED IN HEART, SIGNAL = 1.9  
; OTHER INFORMATION: EXPRESSED IN HELA, SIGNAL = 2.4  
; OTHER INFORMATION: EXPRESSED IN HBL100, SIGNAL = 2.3  
; US-09-864-761-4552

Query Match 3.0%; Score 173.8; DB 9; Length 424;  
Best Local Similarity 93.8%; Pred. No. 4.3e-34;

Matches 181; Conservative 0; Mismatches 12; Indels 0; Gaps 0;

QY 4303 AGCAGAGGATACATGCAATTAACCTGATTAAGCTCCAGCAGGAATGGCTGAACCTAG 4362  
DB 232 AGCAGAGGATACATGCAATTAACCTGATTAAGCTCCAGCAGGAATGGCTGAACCTAG 291  
QY 4363 AAGCTGTGTTGAACAGCAGTGGAGCCGCTTCTTAACAGTACCTTCCATCATTAAGTG 4422  
DB 292 AAGCTGTGTTGAACAGCAGTGGAGCCGCTTCTTAACAGTACCTTCCATCATTAAGTG 351  
QY 4423 ACTCCTGAGCCCTGAGGAGCCTGCGAATCCAGAACAAAGCAGATCAGAAAAAGCAGTAT 4482  
DB 352 ACTCCTGAGCCCTGAGGAGCCTGCGAATCCAGAACAAAGCAGATCAGAAAAAGCAGTAT 411  
QY 4483 TAACTTCACAGAA 4495  
DB 412 ATTGTTGCCAAA 424

Search completed: December 14, 2003, 21:02:03  
Job time : 1682 secs

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